

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 16, 2004, 18:56:15 ; Search time 212.175 Seconds  
(without alignments)  
515.240 Million cell updates/sec

Title: US-10-036-444-2

Perfect score: 1020  
Sequence: 1 MAMWLLILLIMVHPGSCALW.....GTHCHSSDGRGVIPERCP 190

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 02.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	916	89.8	180	1 NCT3_MACMU	Q8MJ02 macaca mla
2	896	87.8	176	1 NCT3_MACFA	P61483 macaca fasc
3	876	85.9	201	1 NCT3_HUMAN	O14931 homo sapien
4	868	85.1	201	1 NCT3_PANTR	P61484 pan troglod
5	606	59.4	192	1 NCT3_RAT	Q8C8D9 rattus norv
6	136.5	13.4	235	2 Q99M11	Q99M11 mus musculu
7	123.5	12.1	313	2 Q6IPU1	Q6IPU1 homo sapien
8	123.5	12.1	313	2 AAH71724	AAH71724 homo sapi
9	120.5	11.8	234	2 Q6GMW3	Q6GMW3 homo sapien
10	119.5	11.7	221	2 Q28090	Q28090 bos taurus
11	117.5	11.5	221	2 Q77631	Q77631 ovis aries
12	115.5	11.3	223	2 Q62859	Q62859 rattus norv
13	114.5	11.2	223	2 Q7TMX1	Q7TMX1 mus musculu
14	112.5	11.0	223	2 Q7JHJ0	Q7JHJ0 macaca neme
15	112.5	11.0	223	2 Q7JHJ2	Q7JHJ2 cercocobus
16	112.5	11.0	223	2 Q9BDC4	Q9BDC4 macaca mla
17	112.5	11.0	223	2 Q9BDN7	Q9BDN7 papio anubi
18	112	11.0	223	1 CTL4_HUMAN	P64410 homo sapien
19	112	11.0	223	2 AAC17066	AAC17066 homo sapi
20	112	11.0	223	2 AAH70162	AAH70162 homo sapi
21	112	11.0	223	2 AAH69566	AAH69566 homo sapi
22	112	11.0	700	2 Q7TSU7	Q7TSU7 mus musculu
23	112	11.0	700	2 BAC33658	BAC33658 m es cell
24	111.5	10.9	226	1 C79A_HUMAN	P11912 homo sapien
25	110.5	10.8	223	2 AAH42741	AAH42741 mus muscu
26	110.5	10.8	234	2 Q6GMV8	Q6GMV8 homo sapien
27	110	10.8	233	2 Q96169	Q96169 homo sapien
28	110	10.8	237	2 Q6DHW4	Q6DHW4 homo sapien
29	109.5	10.7	240	2 Q6MG96	Q6MG96 rattus norv
30	109.5	10.7	240	2 CAE83950	CAE83950 rattus no
31	109	10.7	172	2 Q7LAW3	Q7LAW3 bos taurus

## ALIGNMENTS

### RESULT 1

ID	NCT3_MACMU	STANDARD;	PRT;	180 AA.
AC	Q8MJ02; Q8MJ00; Q8MJ01; Q95JB8;			
DT	05-JUL-2004 (Rel. 44, Created)			
DT	05-JUL-2004 (Rel. 44, Last sequence update)			
DT	01-OCT-2004 (Rel. 45, Last annotation update)			
DE	Natural cytotoxicity triggering receptor 3 precursor (Natural killer cell p30-related protein) (NKP30) (NK-p30).			
GN	Name=NCR3;			
OS	Macaca mulatta (Rhesus macaque).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;			
OC	Cercopithecoidea; Macaca.			
OX	NCBTaxID=9544;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4), AND VARIANT VAL-156.			
RA	LaBonte M.L., Miller J., Letvin N.L.;			
RT	"Molecular cloning of rhesus monkey NKP46 and NKP30 and identification of NKP46SD and NKP30S."			
RT	Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.			
RL	[2]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 4), AND VARIANT VAL-156.			
RA	TISSUE=Lymphoid;			
RC	Rizzi M., Biassoni R.;			
RL	"NCR express by macaca NK cells."			
RL	Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.			
CC	-1- FUNCTION: Cytotoxicity activating receptor that may contribute to the increased efficiency of activated natural killer (NK) cells to mediate tumor cell lysis (By similarity).			
CC	-1- SUBUNIT: Interacts with CD32 (By similarity).			
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).			
CC	-1- ALTERNATIVE PRODUCTS:			
CC	Event=Alternative splicing; Named isoforms=4;			
CC	Name=1;			
CC	IsoId=Q8MJ02-1; Sequence=Displayed;			
CC	Note=No experimental confirmation available;			
CC	Name=2;			
CC	IsoId=Q8MJ02-2; Sequence=VSP 010414;			
CC	Note=No experimental confirmation available;			
CC	Name=3;			
CC	IsoId=Q8MJ02-3; Sequence=VSP 010415, VSP 010416;			
CC	Note=No experimental confirmation available;			
CC	Name=4;			
CC	IsoId=Q8MJ02-4; Sequence=VSP 010417;			
CC	Note=No experimental confirmation available;			
CC	-1- SIMILARITY: Belongs to natural cytotoxicity receptor (NCR) family.			
CC	-1- SIMILARITY: Contains 1 immunoglobulin-like domain.			
CC	-----			
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RC TISSUE=Lymphoid;  
RX PubMed=10562324;  
RA Pende D., Parolini S., Pessino A., Sivori S., Augugliaro R.,  
RA Morelli L., Marceano E., Accame L., Malspina A., Biasoni R.,  
RA Bottino C., Moretta L., Moretta A.;  
RT "Identification and molecular characterization of Nkp30, a novel  
RT triggering receptor involved in natural cytotoxicity mediated by human  
RT natural killer cells";  
RL J. Exp. Med. 190:1505-1516(1999).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM 2), TISSUE SPECIFICITY, AND INTERACTION  
RP WITH CD32.  
RC TISSUE=Peripheral blood;  
RA Sato M., Yabe T., Ohashi J., Tsuchiya N., Hanaoka K., Tokunaga K.,  
RA Juji T.;  
RT "Identification of two novel single nucleotide polymorphisms in the  
RT Nkp30 gene in human natural killer cells";  
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4; 5 AND 6).  
RX MEDLINE=99218514; PubMed=10202016;  
RA Neville M.J., Campbell R.D.;  
RT "A new member of the Ig superfamily and a V-ATPase G subunit are among  
RT the predicted products of novel genes close to the TNF locus in the  
RT human MHC";  
RL J. Immunol. 162:4745-4754 (1999).  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
RC TISSUE=Spleen;  
RX MEDLINE=96422187; PubMed=8824804;  
RA Nalabolu S.R., Shukla H., Nallur G., Parimoo S., Weissman S.M.;  
RT "Genes in a 220-kb region spanning the TNF cluster in human MHC";  
RL Genomics 31:215-222 (1996).  
RN [5]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RX PubMed=14656967; DOI=10.1101/gr.1736803;  
RA Xie T., Rowen L., Aguado B., Ahearn M.E., Madan A., Qin S.,  
RA Campbell R.D., Hood L.;  
RT "Analysis of the gene-dense major histocompatibility complex class III  
RT region and its comparison to mouse";  
RL Genome Res. 13:2621-2636(2003).  
RN [6]  
RP SEQUENCE FROM N.A. (ISOFORM 3).  
RA Shina S., Tamiya G., Oka A., Inoko H.;  
RT "Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region";  
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
RN [7]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC TISSUE=Blood;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,  
RA Butterfield V.S.N., Krzywicki M.I., Skalska U., Smallus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -!- FUNCTION: Cytotoxicity activating receptor that may contribute to  
CC the increased efficiency of activated natural killer (NK) cells to  
CC mediate tumor cell lysis.

CC -!- SUBUNIT: Interacts with CD32.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=6;  
CC Name=1; Synonyms=1C7a;  
CC IsoId=014931-1; Sequence=Displayed;  
CC Note=No experimental confirmation available;  
CC Name=2; Synonyms=1C7c;  
CC IsoId=014931-2; Sequence=VSP\_010413;  
CC Note=No experimental confirmation available;  
CC Name=3; Synonyms=1C7b;  
CC IsoId=014931-3; Sequence=VSP\_010412;  
CC Note=No experimental confirmation available;  
CC Name=4; Synonyms=1C7e;  
CC IsoId=014931-4; Sequence=VSP\_010411;  
CC Note=No experimental confirmation available;  
CC Name=5; Synonyms=1C7f;  
CC IsoId=014931-5; Sequence=VSP\_010411, VSP\_010413;  
CC Note=No experimental confirmation available;  
CC Name=6; Synonyms=1C7d;  
CC IsoId=014931-6; Sequence=VSP\_010411, VSP\_010412;  
CC Note=No experimental confirmation available;  
CC -!- TISSUE SPECIFICITY: Selectively expressed by all resting and  
CC activated NK cells and weakly expressed in spleen.  
CC -!- SIMILARITY: Belongs to natural cytotoxicity receptor (NCR) family.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
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CC  
CC EMBL; AJ223153; CAB54004.1; -;  
CC EMBL; AB055881; BAB78472.1; -;  
CC EMBL; Y14768; CAA75063.1; -;  
CC EMBL; Y14768; CAA75064.1; -;  
CC EMBL; Y14768; CAA75065.1; -;  
CC EMBL; Y14768; CAA75066.1; -;  
CC EMBL; Y14768; CAA75067.1; -;  
CC EMBL; Y14768; CAA75068.1; -;  
CC EMBL; AF031136; AAB86578.1; -;  
CC EMBL; AF031137; AAB86579.1; -;  
CC EMBL; AF031138; AAB86580.1; -;  
CC EMBL; AF129756; RAD18088.1; -;  
CC EMBL; AF000505; BAB63393.1; -;  
CC EMBL; BC052582; AAB52582.1; -;  
CC Genew; HGNC:19077; NCR3.  
CC GO; GO:0006955; P:immune response; NAS.  
CC GO; GO:0006954; P:inflammatory response; NAS.  
CC InterPro; IPR003599; IG.  
CC InterPro; IPR007110; IG-like.  
CC Pfam; PF00047; IG; 1.  
CC SMART; SM00409; IG; 1.  
CC PROSITE; PS00835; IG\_LIKE; 1.  
CC Alternative splicing; Glycoprotein; Immunoglobulin domain; Receptor;  
CC Signal; Transmembrane.  
CC SIGNAL; 1 18  
CC CHAIN; 19 201  
CC  
CC Potential.  
CC Natural cytotoxicity triggering receptor  
CC  
CC 3.  
CC Extracellular (Potential).  
CC Potential.  
CC Cytoplasmic (Potential).  
CC IG-like.  
CC By similarity.  
CC N-linked (GlcNAc...) (Potential).  
CC N-linked (GlcNAc...) (Potential).  
CC Missing (in isoform 4, isoform 5 and  
CC isoform 6).  
CC /FTId=VSP\_010411.  
CC CLTKGPRQLPAVVPAPLPFGGSAHLLPVPVG -> Y  
CC  
CC VARSPPLIC 166 201

FT AKSTLGGPQL (in isoform 3 and isoform 6).  
 FT /FTID=VSP\_010412.  
 FT LTMGPRRLPAPVAPLPPPCGSSAHLPPVPGG -> HC  
 FT HMGTHCHSSDGRGVIPEPRCP (in isoform 2 and  
 FT isoform 5)  
 FT /FTID=VSP\_010413.  
 FT /FTID=VSP\_010413.  
 SQ SEQUENCE 201 AA; 21593 MW; 2855AB46902D429 CRC64;

Query Match 85.9%; Score 876; DB 1; Length 201;  
 Best Local Similarity 89.2%; Pred. No. 9.4e-71;  
 Matches 173; Conservative 2; Mismatches 7; Indels 12; Gaps 2;

QY 1 MAWMLLLILIMVHPGSCALWVSQPPETITLGGSAFLPCSFNASQGLAIGSVTWFRDEV 60  
 DB 1 MAWMLLLILIMVHPGSCALWVSQPPETITLGGSAFLPCSFNASQGLAIGSVTWFRDEV 60  
 QY 61 VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIIYCRVEVLGLGVGTG 120  
 DB 61 VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIIYCRVEVLGLGVGTG 120  
 QY 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAGSTVYQKCHCHMGTHCHSDGP 180  
 DB 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAGSTVYQKCHCHMGTHCHSDGP 180  
 QY 181 R---GVPEPRCP 190  
 DB 173 RRLPAPVAPLPP 186

RESULT 4  
 NCT3 PANTR STANDARD; PRT; 201 AA.  
 ID NCT3 PANTR STANDARD; PRT; 201 AA.  
 AC P61484;  
 DT 05-JUL-2004 (Rel. 44, Created)  
 DT 05-JUL-2004 (Rel. 44, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Natural cytotoxicity triggering receptor 3 precursor (Natural killer  
 DE cell p30-related protein) (NKP30) (NK-p30).  
 GN Name=NCR3;  
 OS Pan troglodytes (Chimpanzee).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
 OX NCBI\_TaxID=9598;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lymphoid;  
 RA Biassoni R.;  
 RL "Characterization of natural killer receptors in chimpanzees.";  
 Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Cytotoxicity activating receptor that may contribute to  
 CC the increased efficiency of activated natural killer (NK) cells to  
 CC mediate tumor cell lysis (By similarity).  
 CC -!- SUBUNIT: Interacts with CD3Z (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
 CC -!- SIMILARITY: Belongs to natural cytotoxicity receptor (NCR) family.  
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
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 CC  
 CC ENMBL; AJ516006; CAD56759.1;  
 DR PROSITE; PS50835; IG LIKE; 1.  
 KW Glycoprotein; Immunoglobulin domain; Receptor; Signal; Transmembrane.  
 FT SIGNAL 1 18 Potential.  
 FT CHAIN 19 201  
 FT DOMAIN 19 135  
 FT TRANSMEM 136 156  
 FT Extracellular (Potential).  
 FT Potential.

FT DOMAIN 157 201 Cytoplasmic (Potential).  
 FT DOMAIN 19 126 Ig-like.  
 FT DISULFID 39 108 By similarity.  
 FT CARBOHYD 42 42 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 121 121 N-linked (GlcNAc...) (Potential).  
 SQ SEQUENCE 201 AA; 21656 MW; 3768ACC768BD749 CRC64;

Query Match 85.1%; Score 868; DB 1; Length 201;  
 Best Local Similarity 88.7%; Pred. No. 4.9e-70;  
 Matches 172; Conservative 2; Mismatches 8; Indels 12; Gaps 2;

QY 1 MAWMLLLILIMVHPGSCALWVSQPPETITLGGSAFLPCSFNASQGLAIGSVTWFRDEV 60  
 DB 1 MAWMLLLILIMVHPGSCALWVSQPPETITLGGSAFLPCSFNASQGLAIGSVTWFRDEV 60  
 QY 61 VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIIYCRVEVLGLGVGTG 120  
 DB 61 VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIIYCRVEVLGLGVGTG 120  
 QY 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAGSTVYQKCHCHMGTHCHSDGP 180  
 DB 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAGSTVYQKCHCHMGTHCHSDGP 180  
 QY 181 R---GVPEPRCP 190  
 DB 173 RRLPAPVAPLPP 186

RESULT 5  
 NCT3 RAT STANDARD; PRT; 192 AA.  
 ID NCT3 RAT STANDARD; PRT; 192 AA.  
 AC Q8CFD9; Q8QW8; Q8CG11;  
 DT 05-JUL-2004 (Rel. 44, Created)  
 DT 05-JUL-2004 (Rel. 44, Last sequence update)  
 DT 01-OCT-2004 (Rel. 45, Last annotation update)  
 DE Natural cytotoxicity triggering receptor 3 precursor (Natural killer  
 DE cell p30-related protein) (NKP30) (NK-p30).  
 GN Name=Ncr3; Synonyms=1C7;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A. AND VARIANTS VAL-7; VAL-19; VAL-82 AND THR-138.  
 RC STRAIN=PVG; TISSUE=Natural killer cells;  
 RX PubMed=12548565; DOI=10.1002/immu.200310008;  
 RA Backman-Petersson E., Miller J.R., Hollyoake M., Aguado B.,  
 RA Butcher G.W.;  
 RL "Molecular characterization of the novel rat NK receptor 1C7.";  
 Eur. J. Immunol. 33:342-351(2003).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Lewis;  
 RX MEDLINE=22168131; PubMed=12180816;  
 RA Hsieh C.L., Obara H., Ogura Y., Martinez O.M., Krams S.M.;  
 RT "NK cells and transplantation.";  
 RN Transpl. Immunol. 9:111-114(2002).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Brown Norway;  
 RX PubMed=15057822; DOI=10.1038/nature02426;  
 RA Gibbs R.A., Weinstein G.M., Metzger M.L., Muzny D.M., Sodergren E.J.,  
 RA Scherer S., Scott G., Steffen D., Worley K.C., Burch P.E., Okwuonu G.,  
 RA Hines S., Lewis L., Deramo C., Delgado O., Dugan-Rocha S., Miner G.,  
 RA Morgan M., Hawes A., Gill R., Holt R.A., Adams M.D., Amanatides P.G.,  
 RA Baden-Tillson H., Barnstead M., Chin S., Evans C.A., Ferreira S.,  
 RA Fiesler C., Glodek A., Gu Z., Jennings D., Kraft C.L., Nguyen T.,  
 RA Frannkoch C.M., Sitter C., Sutton G.G., Venter J.C., Woodage T.,  
 RA Smith D., Lee H.M., Gustafson E., Cahill P., Kana A.,  
 RA Doucette-Stamm L., Weinstein K., Fichtel K., Weiss R.B., Dunn D.M.,  
 RA Green E.D., Blakesley R.W., Bouffard G.G., De Jong P.J., Osoegawa K.,  
 RA Zhu B., Marra M., Schein J., Bosdet I., Fjell C., Jones S.,  
 RA Krywinski M., Mathewson C., Siddiqui A., Wye N., McPherson J.,

RA	Zhao S., Fraser C.M., Shetty J., Shatsman S., Geer K., Chen Y., Abramson S., Nierman W.C., Havlik P.H., Chen R., Durbin K.J., Egan A., Ren Y., Song X.Z., Li B., Liu Y., Qin X., Cawley S., Cooney A.J., D'Souza L.M., Martin K., Wu J.Q., Gonzalez-Garay M.L., Jackson A.R., Kalafus K.J., McLeod M.P., Milosavljevic A., Virk D., Volkov A., Wheeler D.A., Zhang Z., Bailey J.A., Eichler E.E., Tuzun E., Birney E., Mongin E., Ureta-Vidal A., Woodmark C., Zdobnov E., Bork P., Suyama M., Torrents D., Alexandersson M., Trask B.J., Young J.M., Huang H., Wang H., King H., Daniels S., Gietzen D., Schmid J., Stevens K., Vitt U., Wingrove J., Camara F., Mar Alba M., Arill J.F., Guigo R., Smit A., Dubchak I., Rubin E.M., Couronne O., Poliakov A., Hubner N., Ganten D., Goesele C., Hummel O., Kretzler T., Lee Y.A., Monti J., Schulz H., Zimdahl H., Himmelbauer H., Lehrach H., Jacob H.J., Bromberg S., Gullings-Handley J., Jensen-Seaman M.I., Kiteck A.E., Lazar J., Pasko D., Tonelliato P.J., Twigger S., Ponting C.P., Duarte J.M., Rice S., Goodstadt L., Beato S., Ames R.D., Winter E.E., Webber C., Brandt P., Nyakatura G., Adenot M., Chiaronello F., Elmtits L., Eswara P., Hardison R.C., Hou M., Kolbe D., Makova K., Miller W., Nekrutenko A., Riener C., Schwartz S., Taylor J., Yang S., Zhang Y., Lindpaintner K., Andrews T.D., Caccamo M., Clamp M., Clarke L., Curwen V., Durbin R., Eyre E.A., Searle S.M., Cooper G.M., Batzoglu S., Brudno M., Sidow A., Stone E.A., Payseur B.A., Bourque G., Lopez-Otin C., Puente X.S., Chakrabarti K., Chatterji S., Dewey C., Pachter L., Bray N., Yap V.B., Caspi A., Tesler G., Pavzner P.A., Hausler D., Roskin K.M., Baertsch R., Clawson H., Furey T.S., Hinrichs A.S., Karolchik D., Kent W.J., Rosenbloom K.R., Trumbower H., Weirauch M., Cooper D.N., Stenson P.D., Ma B., Brent M., Arumugam M., Shteynberg D., Copley R.R., Taylor M.S., Riechman H., Mudunuri U., Peterson J., Guyer M., Felsenfeld A., Old S., Mockrin S., Collins F., "Genome sequence of the Brown Norway rat yields insights into mammalian evolution.", Nature 428:493-521(2004).	FT	DOVAIN	19	147	3. Extracellular (Potential).
RA	ABRAMSON S., NIERMAN W.C., HAVLIK P.H., CHEN R., DURBIN K.J., EGAN A., REN Y., SONG X.Z., LI B., LIU Y., QIN X., CAWLEY S., COONEY A.J., D'SOUSA L.M., MARTIN K., WU J.Q., GONZALEZ-GARAY M.L., JACKSON A.R., KALAFUS K.J., MCLEOD M.P., MILOSAVLJEVIC A., VIRK D., VOLKOV A., WHEELER D.A., ZHANG Z., BAILEY J.A., EICHLER E.E., TUZUN E., BIRNEY E., MONGIN E., URETA-VIDAL A., WOODMARK C., ZDOBNOV E., BORK P., SUYAMA M., TORRENTS D., ALEXANDERSSON M., TRASK B.J., YOUNG J.M., HUANG H., WANG H., KING H., DANIELS S., GIETZEN D., SCHMID J., STEVENS K., VITT U., WINGROVE J., CAMARA F., MAR ALBA M., ARILL J.F., GUIGO R., SMIT A., DUBCHAK I., RUBIN E.M., COURONNE O., POLIAKOV A., HUBNER N., GANTEN D., GOESELE C., HUMMEL O., KRETZLER T., LEE Y.A., MONTI J., SCHULZ H., ZIMDAHL H., HIMMELBAUER H., LEHRACH H., JACOB H.J., BROMBERG S., GULLINGS-HANDLEY J., JENSEN-SEAMAN M.I., KITECK A.E., LAZAR J., PASKO D., TONELLIATO P.J., TWIGGER S., PONTING C.P., DUARTE J.M., RICE S., GOODSTADT L., BEATO S., AMES R.D., WINTER E.E., WEBBER C., BRANDT P., NYAKATURA G., ADENOT M., CHIARONELLO F., ELMTITS L., ESWARA P., HARDISON R.C., HOU M., KOLBE D., MAKOVA K., MILLER W., NEKRUTENKO A., RIENER C., SCHWARTZ S., TAYLOR J., YANG S., ZHANG Y., LINDPAINTNER K., ANDREWS T.D., CACCAMO M., CLAMP M., CLARKE L., CURWEN V., DURBIN R., EYRE E.A., SEARLE S.M., COOPER G.M., BATZOGLOU S., BRUDNO M., SIDOW A., STONE E.A., PAYSEUR B.A., BOURQUE G., LOPEZ-OTIN C., PUENTE X.S., CHAKRABARTI K., CHATTERJI S., DEWEY C., PACHTER L., BRAY N., YAP V.B., CASPI A., TESLER G., PAVZNER P.A., HAUSLER D., ROSKIN K.M., BAERTSCH R., CLAWSON H., FUREY T.S., HINRICHS A.S., KAROLCHIK D., KENT W.J., ROSENBLUM K.R., TRUMBOWER H., WEIRAUCH M., COOPER D.N., STENSON P.D., MA B., BRENT M., ARUMUGAM M., SHTEYNBERG D., COPELEY R.R., TAYLOR M.S., RIECHMAN H., MUDUNURI U., PETERSON J., GUYER M., FELSENFELD A., OLD S., MOCKRIN S., COLLINS F., "Genome sequence of the Brown Norway rat yields insights into mammalian evolution.", Nature 428:493-521(2004).	FT	TRANSMEM	148	168	Potential.
RA	Hurt P., Walter L., Sudbrak R., Klages S., Mueller I., Shiina T., Inoko H., Lehrach H., Guenther E., Reinhardt R., Himmelbauer H.; "The genomic sequence and comparative analysis of the rat major histocompatibility complex.", Genome Res. 14:631-639(2004).	FT	DOVAIN	169	192	Cytoplasmic (Potential).
RA	CC	CC	CC	CC	CC	IG-like.
RA	CC	CC	CC	CC	CC	By similarity.
RA	CC	CC	CC	CC	CC	I -> V.
RA	CC	CC	CC	CC	CC	I -> V.
RA	CC	CC	CC	CC	CC	I -> V.
RA	CC	CC	CC	CC	CC	A -> V.
RA	CC	CC	CC	CC	CC	A -> T.
RA	CC	CC	CC	CC	CC	A -> V (in Ref. 2).
RA	CC	CC	CC	CC	CC	CONFLICT 135
RA	CC	CC	CC	CC	CC	SEQUENCE 192 AA; 20470 MW; 7FC84FB252D22377 CRC64;
RA	CC	CC	CC	CC	CC	Query Match 59.4%; Score 606; DB 1; Length 192;
RA	CC	CC	CC	CC	CC	Best Local Similarity 64.8%; Pred. NO. 1.8e-46; Indels 8; Gaps 1;
RA	CC	CC	CC	CC	CC	Matches 116; Conservative 25; Mismatches 30;
RA	CC	CC	CC	CC	CC	1 MAMMLLILIMVPGSCALWVSQPFIRTLGSSAFPCSFNASQGLAIGSVTFRDEV 60
RA	CC	CC	CC	CC	CC	1 MAKVLLIVFIMVYAGSCALWVSQPFIRAQGGTTASLPSCFNASRGKAIGSATWYQDKV 60
RA	CC	CC	CC	CC	CC	61 VPGKEVRNGTPEFRORLAPLASSRFLHQBELHTRDVRGHDASIVYCRVEVLGVGTG 120
RA	CC	CC	CC	CC	CC	61 AFGMELSNVTPGRCGRVASFASQFIRGHKAGLLIQDIQSHDARIYVCRVEVLGVGTG 120
RA	CC	CC	CC	CC	CC	121 NGRILWVEKEHPQ-----LGAGTVLLLRAGFYAVSFLSVAGSTVYVYQKCHCMG 171
RA	CC	CC	CC	CC	CC	121 NGRILWVEKEFPQQAASNAPEEAAYTSLLRAGVYALFSLVATSGSVYVYQKCLCHVG 179
RA	CC	CC	CC	CC	CC	RESULT 6
RA	CC	CC	CC	CC	CC	Q99M11 PRELIMINARY; PRT; 235 AA.
RA	CC	CC	CC	CC	CC	Q99M11 STRAIN=Czech II;
RA	CC	CC	CC	CC	CC	Q99M11 01-JUN-2001 (TRENBLrel. 17, Created)
RA	CC	CC	CC	CC	CC	01-JUN-2001 (TRENBLrel. 17, Last sequence update)
RA	CC	CC	CC	CC	CC	01-MAR-2004 (TRENBLrel. 26, Last annotation update)
RA	CC	CC	CC	CC	CC	DE Hypothetical protein.
RA	CC	CC	CC	CC	CC	OS Mus musculus (Mouse).
RA	CC	CC	CC	CC	CC	CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
RA	CC	CC	CC	CC	CC	CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RA	CC	CC	CC	CC	CC	CC NCBI_Taxid=10090;
RA	CC	CC	CC	CC	CC	[1] SEQUENCE FROM N.A.
RA	CC	CC	CC	CC	CC	RA STRAIN=Czech II;
RA	CC	CC	CC	CC	CC	RA TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;
RA	CC	CC	CC	CC	CC	RA MEDLINE=22388257; PubMed=12477932;
RA	CC	CC	CC	CC	CC	RA Strausberg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D.,
RA	CC	CC	CC	CC	CC	RA Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,
RA	CC	CC	CC	CC	CC	RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA	CC	CC	CC	CC	CC	RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA	CC	CC	CC	CC	CC	RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA	CC	CC	CC	CC	CC	RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Pange C.,
RA	CC	CC	CC	CC	CC	RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA	CC	CC	CC	CC	CC	RA Bosak S.A., McSwan P.J., McKernan K.J., Velek J.A., Gunaratne P.H.,
RA	CC	CC	CC	CC	CC	RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	CC	CC	CC	CC	CC	RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	CC	CC	CC	CC	CC	RA Whiting J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA	CC	CC	CC	CC	CC	RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	CC	CC	CC	CC	CC	RA Rodriguez A.C., Grimwood J., Schumz J., Myers R.M., Butterfield Y.S.,
RA	CC	CC	CC	CC	CC	RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA	CC	CC	CC	CC	CC	RA Jones S.J., Marra M.A.;
RA	CC	CC	CC	CC	CC	RA "Generation and initial analysis of more than 15,000 full-length human
RA	CC	CC	CC	CC	CC	RA and mouse cDNA sequences.",
RA	CC	CC	CC	CC	CC	RA Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RA	CC	CC	CC	CC	CC	[2]
RA	CC	CC	CC	CC	CC	RA SEQUENCE FROM N.A.
RA	CC	CC	CC	CC	CC	RA STRAIN=Czech II;
RA	CC	CC	CC	CC	CC	RA TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;
RA	CC	CC	CC	CC	CC	RA Strausberg R.;
RA	CC	CC	CC	CC	CC	RA Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.





## RESULT 11

O97631 PRELIMINARY; PRT; 221 AA.  
 AC O97631, 10, Created)  
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Cytotoxic T-lymphocyte-associated protein 4.  
 GN Name=CTLA-4;  
 OS Ovis aries (Sheep).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Caprinae; Ovis.  
 OX NCBI\_TaxID=9940;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9309828; PubMed=10380709;  
 RA Chaplin P.J., Pietrala L.N., Scheerlinck J.P.;  
 RT "Cloning and sequence comparison of sheep CD28 and CTLA-4.";  
 RL Immunogenetics 49:583-584(1999).  
 DR EMBL; AF092740; AAD04380.1; -.  
 DR HSSP; P16410; 1185.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR008096; CTLA4.  
 DR InterPro; IPR003599; IG.  
 DR Pfam; PF00047; IG; 1.  
 DR PRINTS; PR01720; CTLANTIGEN4.  
 DR SMART; SM00409; IG; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 SQ SEQUENCE 221 AA; 24490 MW; D317B9D5557BA6FB CRC64;

Query Match 11.5%; Score 117.5; DB 2; Length 221;  
 Best Local Similarity 28.0%; Pred. No. 0.019;  
 Matches 45; Conservative 25; Mismatches 80; Indels 11; Gaps 4;  
 QY 6 LLLILIMVHPGSCALWVQPPFIRTELGSSAFPCSFNASQRLAIGSVTWFDEVPGKE 65  
 DB 23 LFFLLFIPVSKGNVTPPPVVLASSRGVASFCEYESS-GKADVVTVLRKAGIQVTE 81  
 QY 66 VRNGTPEFRGRFLAPLASSRFL---HDSQAEHLHVRDVGHDASIVYCRVEVL---GLGVGT 119  
 DB 82 VCACTYVVEDELTDSSCGISRGKNVLTIOGLRANDTGLVCKVELMYPPYMGSE 141  
 QY 120 GNGTRLVVEKHPOLGAGTVLLRA-----GFYAVSFLSVAV 156  
 DB 142 GNGRQIYVIDPEPCPDSDFLWILAAVSSGLFFYSFLITAV 182

## RESULT 12

O62859 PRELIMINARY; PRT; 223 AA.  
 AC O62859, 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Cytotoxic T-lymphocyte associated protein-4 precursor.  
 GN Name=CTLA-4;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96134012; PubMed=8550107;  
 RA Oaks M.K., Penwell R.T., Tector A.J.;  
 RT "Nucleotide sequence of the ACI rat CTLA-4 molecule.";  
 RL Immunogenetics 43:173-174(1996).  
 DR EMBL; U37121; AAC52502.1; -.  
 DR HSSP; P09793; 1DQT.  
 DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR008096; CTLA4.  
 DR InterPro; IPR003599; IG.  
 DR Pfam; PF00047; IG; 1.  
 DR PRINTS; PR01720; CTLANTIGEN4.  
 DR SMART; SM00409; IG; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 KW Signal.  
 FT SIGNAL 1 37 Potential.  
 FT CHAIN 38 223 Potential.  
 SQ SEQUENCE 223 AA; 24858 MW; C19EE4F242C6A87B CRC64;

Query Match 11.3%; Score 115.5; DB 2; Length 223;  
 Best Local Similarity 28.7%; Pred. No. 0.03;  
 Matches 48; Conservative 26; Mismatches 72; Indels 21; Gaps 7;

QY 5 LLLILIMVHPGSCALWVQPPFIRTELGSSAFPCSFNASQRLAIGSVTWFDEV 60  
 DB 24 VLLSLFPIFSEAIQTQPSVVLASSHGVSFPCSEYASSHTDVRVTVLRQT--NDQV 81  
 QY 61 VPGKEVRNGTPEFRGELA-----PLASSRFLHDHQAELHVRDVGHDASIVYCRVEVL--- 113  
 DB 82 T---EVCATTFVTKNTLGLDDPFCSGTF-NESRVNLTIOGLRAADTGLYFCVELAYPP 137  
 QY 114 GLGVGTGNGTRLVVEKHPOLGAGTVLLRA-----GFYAVSFLSVAV 156  
 DB 138 PVFVGMGNGTQIYVIDPEPCPDSDFLWILAAVSSGLFFYSFLITAV 184

## RESULT 13

Q7TMX1 PRELIMINARY; PRT; 223 AA.  
 AC Q7TMX1, 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Cytotoxic T-lymphocyte-associated protein 4.  
 GN Name=CTLA4;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22389257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Schuler G.D.,  
 RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haefl F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettner M., Maman A., Rodriguez S., Sanchez A.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=C57BL/6Ncr; TISSUE=Hematopoietic Stem Cell;  
 RA Strausberg R.;  
 RL Submitted (May-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC052683; AAH52683.1; -.

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DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PSS0835; IG-LIKE; 1.
SQ SEQUENCE 223 AA; 25035 MW; EE8E4C77E6A04549 CRC64;

Query Match 11.2%; Score 114.5; DB 2; Length 223;
Best Local Similarity 27.5%; Pred. No. 0.037;
Matches 46; Conservative 25; Mismatches 79; Indels 17; Gaps 6;

QY 3 WMLLILIMVHFGSCALMWSQPPEIRTLGSSAFPLPCSFNASQGRLAIGSVTWFRD-----58
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 22 FVALLTLFIPVFSKAMHVAQPAVVLANSRGIAFVCEY-ASPGKATEVRVTVLROADSQ 80
QY 59 --EWPQKEVRNGTPPEGRGLAPLASSRFLHDHQAELHIRDVRGHDAIYVCRVEVL---113
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 81 MTEVCATTFTEKNTVGFLD--YFPCSGTF--NESRVNLTIQGLRAVDTGFLCKVELMYPP 137
QY 114 GLGVGTGNGTRLVVEKEHPQLGAGTVL-----LLRAGFYAVSFLSVAV 156
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 138 PYFVGNGNGRIYVIDPEPCDSDFLWLILVAVSLGLFFYSFLVTAV 184

RESULT 14
Q7JHJ0 PRELIMINARY; PRT; 223 AA.
ID Q7JHJ0
AC Q7JHJ0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE DE CD152 protein precursor.
GN Name=CTLA-4;
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Macaca.
OC NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21383618; PubMed=11491535;
RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
RT Fas/Fas-ligand and co-stimulatory molecules.";
RL Immunogenetics 53:315-328(2001).
DR EMBL; AF344848; AAK37608.1; -
DR InterPro; IPR008096; CTLA4.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IG V.
DR PRINTS; PR01720; CTLANTIGEN4.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 223 AA; 24683 MW; BDE42248A00398FA CRC64;

Query Match 11.0%; Score 112.5; DB 2; Length 223;
Best Local Similarity 27.6%; Pred. No. 0.055;
Matches 47; Conservative 23; Mismatches 77; Indels 23; Gaps 5;

QY 3 WMLLILIMVHFGSCALMWSQPPEIRTLGSSAFPLPCSFNASQGRLAIGSVTWFRDVEVP 62
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 22 YTLFSLFLFIPVFSKAMHVAQPAVVLANSRGIAFVCEY-ASPGKATEVRVTVLROADSQ 80
QY 63 GKEVRNGTPEFGRGLAPLASSRFLHD-----HQAELHIRDVRGHDAIYVCRVEVL 113
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 81 VTEVCAATYMGNELT-----FLDSDICTGSSGNQVNLTIQGLRAMDTGLYICKVELM 134
QY 114 ---GLGVGTGNGTRLVVEKEHPQLGAGTVLLRA-----GFYAVSFLSVAV 156
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 135 YPPPYMGIGNGTQIYVIDPEPCDSDFLWLILAAVSSGLFFYSFLLTAV 184

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 16, 2004, 18:56:40 ; Search time 39.3103 Seconds  
(without alignments)  
465.048 Million cell updates/sec

Title: US-10-036-444-2  
Perfect score: 1020  
Sequence: 1 YANWLLILLIMVHPGSCALW.....GTHCHSSDGRGVIPRCP 190

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Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

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Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : FIR\_79:\*  
1: Pir1:\*  
2: Pir2:\*  
3: Pir3:\*  
4: Pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	118	11.6	136	B45893	T-cell receptor al
2	117.5	11.5	132	A24402	T-cell receptor al
3	116	11.4	146	S26408	T-cell receptor be
4	115.5	11.3	232	S25756	Ig lambda chain -
5	111.5	10.9	226	A46477	membrane-bound imm
6	111	10.9	233	S25747	Ig lambda chain -
7	110	10.8	223	T09536	cytotoxic T-lympho
8	108.5	10.6	223	A29063	Ig lambda chain -
9	108	10.6	235	S25749	Ig lambda chain -
10	107.5	10.5	138	C27577	T-cell receptor al
11	106.5	10.4	131	D24032	T-cell receptor al
12	106.5	10.4	131	E24032	T-cell receptor al
13	106	10.4	132	1	T-cell receptor al
14	105	10.3	131	F45893	Ig lambda chain v
15	104.5	10.2	132	S09713	CTLA-4 precursor -
16	103.5	10.1	223	I46696	T-cell receptor al
17	103	10.1	129	A42692	T-cell receptor al
18	102.5	10.0	110	B24032	T-cell receptor de
19	101.5	10.0	139	S36385	T-cell receptor al
20	101	9.9	120	S54487	T-cell receptor al
21	101	9.9	235	S14675	Ig lambda chain -
22	100.5	9.9	1694	S50065	sialoadhesin - mou
23	100	9.8	110	A24032	T-cell receptor al
24	99.5	9.8	271	A53268	T-cell receptor al
25	99	9.7	130	A31211	T-cell receptor al
26	98.5	9.7	128	S24319	Ig lambda chain pr
27	98.5	9.7	152	S21826	T-cell receptor be
28	98.5	9.7	236	S25746	Ig lambda chain -
29	98.5	9.7	247	A55717	myelin/oligodendro

Query Match 11.6%; Score 118; DB 2; Length 136;  
Best Local Similarity 27.9%; Pred. No. 0.0017;  
Matches 41; Conservative 22; Mismatches 42; Indels 42; Gaps 9;  
QY 4 MILLILIMV-----HPGSCALWVQPPETLTGSSAFPLPCSNAGRLAIGSVTW 56  
DB 8 LLVILLASVDLRQPAHSG-----AEPASLPVPEGAASLGCTYSDNSLY----FTWY 57  
QY 57 RDEVVPGKEVRNGTPEF-----RGLAPLASSRFLHDHQAELHIRDVRGHDASI 105  
DB 59 RQ--YPGK-----GPEFLQVYANNKKEGFT--AQSNKINKH-VSLRIRDSFSDSAT 107  
QY 106 YVCVEVLGLVGT----GNGTRLVVE 128  
DB 108 YLCAVDTTTATTAGTKLTFTGEGTRLIVK 134  
RESULT 2  
A24402  
T-cell receptor alpha chain precursor V region (C5) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 23-Aug-1987 #sequence\_revision 23-Aug-1987 #text\_change 30-May-1997  
C;Accession: A24402  
R;Becker, D.N.; Patten, P.; Chien, Y.; Yokota, T.; Eschhar, Z.; Giedlin, M.; Gascoigne, I.  
Nature 317, 430-434, 1985  
A;Title: Variability and repertoire size of T-cell receptor V-alpha gene segments.  
A;Reference number: A93368; MUID:86014379; PMID:2995827  
A;Accession: A24402  
A;Molecule type: mRNA  
A;Residues: 1-132 <BEC>  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: T-cell receptor  
Query Match 11.5%; Score 117.5; DB 2; Length 132;

ALIGNMENTS

RESULT 1  
B45893  
T-cell receptor alpha chain precursor V region (BTA29) - bovine  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 20-Jun-2000  
C;Accession: B45893  
R;Ishiguro, N.; Tanaka, A.; Shinagawa, M.  
Immunogenetics 31, 57-60, 1990  
A;Title: Sequence analysis of bovine T-cell receptor alpha chain.  
A;Reference number: A45893; MUID:90129157; PMID:2137108  
A;Accession: B45893  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-136 <LSH>  
A;Cross-references: GB:D90011; NID:g217610; PIDN:BAAL4061.1; PID:g217611  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: T-cell receptor

30	98.5	9.7	526	2	S70587	butyrophilin presu
31	96	9.4	131	1	L6HUEB	Ig lambda chain pr
32	96	9.4	131	2	D24402	T-cell receptor al
33	95.5	9.4	140	2	PH0134	Ig lambda chain pr
34	95.5	9.4	218	2	B47112	myelin/oligodendro
35	94.5	9.3	108	2	JH0342	T-cell receptor al
36	94.5	9.3	186	2	S08614	cytotoxic T-lympho
37	93.5	9.2	247	2	S58394	myelin/oligodendro
38	93	9.1	117	2	I68824	T-cell receptor al
39	93	9.1	132	2	D45893	T-cell receptor al
40	93	9.1	246	1	A32999	myelin P0 protein
41	93	9.1	267	1	RWMS08	T-cell receptor al
42	92.5	9.1	136	2	S42610	ARMVlambda protein
43	92.5	9.1	139	2	S36302	T-cell receptor de
44	92.5	9.1	403	2	I32590	m33-B isoform - mo
45	92	9.0	129	2	A30554	Ig lambda chain pr



A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-88 'E', 128-226 <HAS>  
A;Cross-references: GB:979248; NID:g1087006; PIDN:CAA60653.1; PID:g1087007  
submitted to the EMBL Data Library, December 1994  
A;Reference number: S51112  
A;Accession: S51113  
A;Molecule type: mRNA  
A;Residues: 1-88 'E', 128-226 <KOY>  
A;Cross-references: EMBL:X93540; NID:g620080; PIDN:CAA58523.1; PID:g620081  
C;Genetics:  
A;Gene: GDB:IGA; mb-1; CD79a  
A;Cross-references: GDB:133778; OMIM:600352  
A;Map position: 19q13.2-19q13.2  
A;Introns: 27/1; 127/1; 166/3; 190/1  
C;Complex: disulfide-linked heterodimer with Ig-beta; heterodimer associates non-covalently  
C;Keywords: alternative splicing; signal sequence #status predicted <SIG>  
F:1-32/Domain: signal sequence #status predicted <SIG>  
F:33-226/Product: membrane-bound immunoglobulin Ig-alpha chain #status predicted <WAT>  
F:33-143/Domain: extracellular #status predicted <EXT>  
F:144-165/Domain: transmembrane #status predicted <TM>  
F:166-226/Domain: intracellular #status predicted <CYT>  
F:57,63,73,88,97,112/Binding site: carbohydrate (Asn) (covalent) #status predicted  
P:57,63,73,88,97,112/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.9%; Score 111.5; DB 2; Length 226;  
Best Local Similarity 28.0%; Pred. No. 0.011;  
Matches 47; Conservative 24; Mismatches 70; Indels 27; Gaps 8;

QY 4 MLILIMVHVGSCALVSO-PPPIRTLEGSSAFPCSFNASQGRLAIGSVTWFRDEVVP 62  
Db 18 LFLSAYVLGPGCOALWKKVPSLVSLGDAHFQCPHNSNN-ANVTWR-VLH 71  
QY 63 GKEVRNGT-PEFGRGLAPLASSRFLHDHQAELHIRDVRGHDSIYVCRVEVL-GLGVGTG 120  
Db 72 G---NVTWPDEFGLP-----GEDPNTLIIQNVKSHGIIYVCRVQEGNESYQOS 118  
QY 121 NGTILVVEKEHPQ---LGRGTV-LLLRAGFYAVSFLSVAGSVTVYQ 163  
Db 119 CGTYLRVQPPRPFDFMDGEGTKNRIITAEQIILFCAVPGTLLFLR 166

RESULT 6  
S25747  
Ig lambda chain - human  
C;Species: Homo sapiens (man)  
C;Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C;Accession: S25747  
R;Combrinato, G.; Klobbeck, H.G.  
Eur. J. Immunol. 21, 1513-1522, 1991  
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam  
A;Reference number: S16439; MUID:91257162; PMID:1904362  
A;Accession: S25747  
A;Status: preliminary; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-233 <COM>  
A;Cross-references: EMBL:X57812; NID:g337723; PIDN:CAA40949.1; PID:g33724  
A;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F:148-216/Domain: immunoglobulin homology <IMW>

Query Match 10.9%; Score 111; DB 2; Length 233;  
Best Local Similarity 28.0%; Pred. No. 0.013;  
Matches 49; Conservative 24; Mismatches 60; Indels 42; Gaps 10;

QY 1 MAWMLLLIMVH-PCSCALVW-SQPPPIRTLEGSSAFPCSFNASQGRLAIGSVTWFR 57  
Db 1 MAWTVLLGLLSHCSTSVTSYVLTQPPSVAPGAARITCG-----GINTASKSVHWYQ 55  
QY 58 DB-----VVPGEKVR-NGTPE-FGRGLAPLASSRFLHDHQAELHIRDVRGHDSIYVC 108  
Db 56 QKPGQAPVLVYVGDSDRSGIPERFSGNS-----GNTATLINISRVEAGDEAAAYC 106

QY 109 RV-EVLGLVGTGNGTRLVV-----EKEHPOLGAGTVLLLRAGEY 147  
Db 107 QWMDSSDHVYVFGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFY 161

RESULT 7  
T09536  
cytotoxic T-lymphocyte protein 4 - human  
C;Species: Homo sapiens (man)  
C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 21-Jul-2000  
C;Accession: T09536  
R;Harper, K.; Balzano, C.; Rouvier, E.; Mattei, M.G.; Luciani, M.F.; Golstein, P.  
J. Immunol. 147, 1037-1044, 1991  
A;Title: CTLA-4 and CD28 activated lymphocyte molecules are closely related in both mou  
A;Reference number: I49584; MUID:91318145; PMID:1713603  
A;Accession: T09536  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-223 <HAR>  
A;Cross-references: EMBL:L15006; NID:g291928; PIDN:AAB59385.1; PID:g291929  
C;Genetics:  
A;Gene: CTLA4  
A;Map position: 2q33  
C;Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology  
C;Keywords: T-cell; transmembrane protein

Query Match 10.8%; Score 110; DB 2; Length 223;  
Best Local Similarity 28.0%; Pred. No. 0.015;  
Matches 47; Conservative 22; Mismatches 75; Indels 24; Gaps 6;

QY 6 LLILIMVHVGSC-ALWVSQPPPIRTLEGSSAFPCSFNASQGRLAIGSVTWFRDEVVPCK 64  
Db 24 LLFFLLFIPVFCAMHVAQPAVVLASSRGIASFVCEY-ASPGKATEVRVTVLROADSQVT 82  
QY 65 EYRNGTPEFGRGLAPLASSRFLHD-----HQAELHIRDVRGHDSIYVCRVEVL- 113  
Db 83 EYCAATYTGNELT-----FLDDISCTGTSSGNNVITIQGLRANMTGLYICKVELMYP 136  
QY 114 -GLGVGTGNGTRLVVEKEHPOLGAGTVLLLR-----GFYAVSFLSVAV 156  
Db 137 PYYIIGIGNGTIYVIDPECPDSDFLWILAAVSSGLFFYSFLTAV 184

RESULT 8  
A29063  
cytotoxic T-lymphocyte protein 4 - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 21-May-1988 #sequence\_revision 21-May-1988 #text\_change 09-Jul-2004  
C;Accession: A29063; I49622  
R;Brunet, J.F.; Denizot, F.; Luciani, M.F.; Roux-Dosseto, M.; Suzan, M.; Mattei, M.G.;  
Nature 328, 267-270, 1987  
A;Title: A new member of the immunoglobulin superfamily--CTLA-4.  
A;Reference number: A29063; MUID:8758259; PMID:3496540  
A;Accession: A29063  
A;Molecule type: mRNA  
A;Residues: 1-223 <BRU>  
A;Cross-references: UNIPROT:P09793; GB:X05719; NID:g50592; PIDN:CAA29191.1; PID:g50593  
R;Harper, K.; Balzano, C.; Rouvier, E.; Mattei, M.G.; Luciani, M.F.; Golstein, P.  
J. Immunol. 147, 1037-1044, 1991  
A;Title: CTLA-4 and CD28 activated lymphocyte molecules are closely related in both mou  
A;Reference number: I49584; MUID:91318145; PMID:1713603  
A;Accession: I49622  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-36 <RES>  
A;Cross-references: GB:M74362; NID:g192833; PIDN:AAA37489.1; PID:g553903  
C;Genetics:  
A;Gene: CtlA-4  
A;Map position: 1, band C  
C;Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology  
C;Keywords: transmembrane protein

Query Match 10.6%; Score 108.5; DB 2; Length 223;

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Best Local Similarity 26.9%; Pred. No. 0.02;
Matches 45; Conservative 26; Mismatches 79; Indels 17; Gaps 6;

QY 3 MWLLILLIHWPGSCALWVSOPPEIRTLGSSAFPLPCSFNASQGRLAIGSVTWFRD---- 58
Db 22 FVALLTLFLFIPVFSAGIQTPSVVVLASGHGVAFFPCPESSHNTDEV-RVTLRQNTDQ 80
QY 59 --EVVPGKEVRNGTPEFRGRILAPLASSRFLHDHQAELHIRDVGRHDASIVVCRVEVL--- 113
Db 81 MTEVCATFTTEKNTVGFLD--YPCSGTF-NESRVNLTIQGLRAVDITGLICKVELMYPP 137
QY 114 GLGVGTGNGTRLVVEKEHPQLGAGTVL-----LLRAGFYAVSFVLVAV 156
Db 138 PYFVGMGNGTQIYVIDPEPCDPSDFLLWILVAVSLGLFFYSFLVSAV 184

RESULT 9
S25749
Ig lambda chain - human
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S25749
R:Combratio, G.; Klobbeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A:Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A:Reference number: S16439; MUID:91257162; PMID:1904362
A:Accession: S25749
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-235 <COM>
A:Cross-references: EMBL:X57814; NID:933727; PIDN:CAA40951.1; PID:933728
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:150-218/Domain: immunoglobulin homology <IMM>

Query Match 10.6%; Score 108; DB 2; Length 235;
Best Local Similarity 25.1%; Pred. No. 0.024;
Matches 45; Conservative 26; Mismatches 60; Indels 48; Gaps 10;

QY 1 MAMWLLILLIHWPGS---CALWVSOPPEIRTLGSSAFPLPCSFNASQGRLAIGSVTWFR 57
Db 1 MAMWLLILLIHWPGS---CALWVSOPPEIRTLGSSAFPLPCSFNASQGRLAIGSVTWFR 58
QY 58 DEVVPGKEVR-----NGTPE-FRGRILAPLASSRFLHDHQAELHIRDVGRHDASTY 106
Db 59 Q--TPGQAPRTLMYNTNRSGVDFRFGSIL-----GNKSALTITGAQADESDY 107
QY 107 VCRVEVLGLVGT---GNGTRLVY-----EKEHPQLGAGTVLLLRAGFY 147
Db 108 YC---VLYMGRIIVFGGKTAVLGQKAPASVTLFPPSPSEELQANKATVLCILSDFY 163

RESULT 10
C27577
T-cell receptor alpha chain V region (5/10-20D) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 30-May-1997
C:Accession: C27577
R:Iwamoto, A.; Ohashi, P.S.; Pircher, H.; Walker, C.L.; Michalopoulos, E.E.; Rupp, F.; H
J. Exp. Med. 165, 591-600, 1987
A:Title: T cell receptor variable gene usage in a specific cytotoxic T cell response. P
A:Reference number: A27557; MUID:87139812; PMID:3493320
A:Accession: C27577
A:Molecule type: mRNA
A:Residues: 1-138 <IWA>
A:Accession: C27557
A:Molecule type: mRNA
A:Residues: 22-138 <IW2>
A:Cross-references: EMBL:X05733
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor

Query Match 10.5%; Score 107.5; DB 2; Length 138;

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Best Local Similarity 31.9%; Pred. No. 0.015;
Matches 38; Conservative 17; Mismatches 45; Indels 19; Gaps 7;

QY 21 VSQPEIRTL-EGSSAFPLPCSFNASQGRLAIGSVTWFRDEVVPGKEVR-----NGTPE 72
Db 24 VQSPESLIVPEGAMTSLNCTFSDSASQV----FAMYRQH--SGKAPKALMSIFSGEKE 77
QY 73 FEGRLAPLASSRFLHDHQAELHIRDVGRHDASIVVCRVEVL-GLGVGTGNGTRLVVEKE 130
Db 78 -EGRTIHLNKASLH---FSLHIRDSPSDSALYLCVSMTGKYKVFSGTRLULVSPD 132

RESULT 11
D24092
T-cell receptor alpha chain precursor V region (B10) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 19-Nov-1988 #sequence_revision 01-Dec-2000 #text_change 11-Jan-2002
C:Accession: D24092; S03507
R:Fink, P.J.; Matis, L.A.; McElligott, D.L.; Bookman, M.; Hedrick, S.M.
Nature 321, 219-226, 1986
A:Title: Correlations between T-cell specificity and the structure of the antigen recept
A:Reference number: A93380; MUID:86230843; PMID:3012351
A:Accession: D24092
A:Molecule type: mRNA
A:Residues: 1-131 <FIN>
R:Wimoto, A.; Mjolsness, S.; Hood, L.
Nature 316, 832-836, 1985
A:Title: Genomic organization of the genes encoding mouse T-cell receptor alpha-chain.
A:Reference number: S03503; MUID:85296332; PMID:2993908
A:Accession: S03507
A:Molecule type: DNA
A:Residues: 111-130 <WIN>
A:Cross-references: EMBL:X03057; NID:954519; PIDN:CAA26864.1; PID:G1334131
A:Note: this sequence was determined from the germline gene
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-131/Product: T-cell receptor alpha chain V region B10 #status predicted <MAT>
F:36-109/Domain: immunoglobulin homology <IMM>

Query Match 10.4%; Score 106.5; DB 2; Length 131;
Best Local Similarity 29.6%; Pred. No. 0.017;
Matches 37; Conservative 19; Mismatches 42; Indels 27; Gaps 7;

QY 21 VSQPEIRTL-EGSSAFPLPCSFNASQGRLAIGSVTWFR-----RDEVVPGKEVRNGTPEFRG 75
Db 24 VEQSPSALSLEHGTGSLRCNFTTT-----MRAVQWFRKNSRGSILNLFYLSAGTKE-NG 77
QY 76 RLAPLASSRFLHDHQAELHIRDVGRHDASIVVCRVEVLGLGVGTGNGTRLVVEKEHPQLG 135
Db 78 RLKSAFDSK---ERYSTLHIRDAQLEDSTGYFCAAE-----ATSSQKLV-----FG 121
QY 136 AGTVL 140
Db 122 QGTIL 126

RESULT 12
E24092
T-cell receptor alpha chain precursor V region (4.C3) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 21-Jan-2000
C:Accession: E24092
R:Fink, P.J.; Matis, L.A.; McElligott, D.L.; Bookman, M.; Hedrick, S.M.
Nature 321, 219-226, 1986
A:Title: Correlations between T-cell specificity and the structure of the antigen recept
A:Reference number: A93380; MUID:86230843; PMID:3012351
A:Accession: E24092
A:Molecule type: mRNA
A:Residues: 1-131 <FIN>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor
F:1-20/Domain: signal sequence #status predicted <SIG>

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F/21-131/Product: T-cell receptor alpha chain V region 4.C3 #status predicted <MAT>  
F/36-109/Domain: immunoglobulin homology <IMM>

Query Match 10.4%; Score 106.5; DB 2; Length 131;  
Best Local Similarity 29.8%; Pred. No. 0.017; Indels 27; Gaps 7;  
Matches 37; Conservative 19; Mismatches 42

QY 21 VSQPEIRTL-EGSSAFPCSFNASQGRLAIGSVTWTF-----RDEVVPGKEVRNGTPEFRG 75  
DB 24 VEQSPSALS-HEGTGSAIRCNTFTT-----MRAVQFRKNSRGLNLFVYASGTKE-NG 77  
QY 76 RLAPLASSRFLHDHQAELHIRDVGRHDASIYCRVEVLGVGTGNGTRLVVEKEHPQLG 135  
DB 78 RLKSAFDSK---ERYSTLHIDAQLEDSGTFFCAAE-----STSSGQKLV-----FG 121  
QY 136 AGTVL 140  
DB 122 QGRIL 126

## RESULT 13

RWMSGAV  
T-cell receptor alpha chain precursor V region (2B4) - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 28-May-1986 #sequence\_revision 28-May-1986 #text\_change 09-Jul-2004  
C/Accession: A02015  
C/Chien, Y.; Becker, D.M.; Lindsten, T.; Okamura, M.; Cohen, D.I.; Davis, M.M.  
Nature 312, 31-35, 1984  
A/Title: A third type of murine T-cell receptor gene.  
A/Reference number: A93344; MUID:85036634; PMID:6548551  
A/Accession: A02015  
A/Molecule type: mRNA  
A/Residues: 1-132 <CHI>  
A/Cross-references: UNIPROT:P01739  
A/Experimental source: hybridoma 2B4, clone T11  
C/Suprafamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: Glycoprotein; heterotetramer; receptor; T-cell  
F/1-20/Domain: signal sequence #status predicted <SIG>  
F/21-132/Product: T-cell receptor alpha chain V region (2B4) #status predicted <MAT>  
F/21-113/Region: V segment  
F/114-117/Region: D segment  
F/118-132/Region: J segment  
F/42/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 10.4%; Score 106; DB 1; Length 132;  
Best Local Similarity 25.8%; Pred. No. 0.019; Indels 48; Gaps 9;  
Matches 40; Conservative 22; Mismatches 45

QY 3 WMLLILIMVHPGSCALWVS-----QPPEIRTEGSSAFPCSFNASQGRLAIGSVTW 55  
DB 12 WLLL-----NWNSQNVQSPESLIIVPEGARTSLNCTFSDSASQY---FWW 55  
QY 56 PRDEVVPGKEVR-----NGTPFERGLAPLASSRFLHDHQAELHIRDVGRHDASIYVC 108  
DB 56 YROH--SGKAPKALMSIFSNGEXE-EGKFTIHLKASLH---FSLHIRDSPDSALYLC 109  
QY 109 RVEVLGLGVGTGNGTRLVVEKEHPQLGAGTVLLIR 143  
DB 110 AVTLVG-----GSGNKLI-----FGTGILLSVK 132

## RESULT 14

F45893  
T-cell receptor alpha chain precursor V region (BTA25) - bovine  
C/Species: Bos primigenius taurus (cattle)  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 20-Jun-2000  
C/Accession: F45893  
C/Rishiguro, N.; Tanaka, A.; Shinagawa, M.  
Immunogenetics 31, 57-60, 1990  
A/Title: Sequence analysis of bovine T-cell receptor alpha chain.  
A/Reference number: F45893; MUID:90129157; PMID:2137108  
A/Accession: F45893  
A/Status: preliminary

A/Molecule type: mRNA  
A/Residues: 1-131 <ISH>  
A/Cross-references: GB:D90015; NID:g217618; PIDN:BAA14065.1; PID:g217619  
C/Suprafamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: T-cell receptor  
F/36-109/Domain: immunoglobulin homology <IMM>

Query Match 10.3%; Score 105; DB 2; Length 131;  
Best Local Similarity 30.3%; Pred. No. 0.024; Indels 26; Gaps 8;  
Matches 36; Conservative 23; Mismatches 34

QY 21 VSQPEIRTL-EGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKE-----VRNGTPEF 73  
DB 24 VEQSPSVLSLQEGGANSTLRCNFSDT-----VDSVQWFQON--PGALTLTFFIASGYK- 75  
QY 74 RGRLAPLASSRFLHDHQAELHIRDVGRHDASIYCRVEVLGLGVGT-----GNGTRLV 127  
DB 76 NERMSTVNSK---ERYSTLHTITASQLEDAATYLCVD---LGSNGRLVFGKGTRELAV 128

## RESULT 15

S09713  
Ig lambda chain V region - human  
C/Species: Homo sapiens (man)  
C/Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004  
C/Accession: S09713  
C/Rhughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.  
Biochem. J. 268, 135-140, 1990  
A/Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domains  
A/Reference number: S09710; MUID:90262535; PMID:2111699  
A/Accession: S09713  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-132 <HUG>  
A/Cross-references: UNIPROT:Q8N355  
C/Suprafamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/34-110/Domain: immunoglobulin homology <IMM>

Query Match 10.2%; Score 104.5; DB 2; Length 132;  
Best Local Similarity 29.8%; Pred. No. 0.026; Indels 25; Gaps 8;  
Matches 42; Conservative 20; Mismatches 54

QY 1 MAWMLLILIMVH-FGSCALWV-SQPPEIRTEGSSAFPCSFNASQGRLAIGSVTWFRD 58  
DB 1 MAWTVLL-LGILLSHCITGVSIVLTQPPSVVAPGQTARITC--GGTSNNICKSVHWYQQ 58  
QY 59 E-----VPGKEVR-NGTPE-FGRLAPLASSRFLHDHQAELHIRDVGRHDASIYVC 109  
DB 59 KPGQAPVLVYVGASDRPGIPERFSGNS-----GNTATLTISRVAAGDEADYYCQ 109  
QY 110 V---EVLGLGVGTGNGTRLV 127  
DB 110 VWDSSAHPGVVFGGTKLTV 130

Search completed: November 16, 2004, 19:15:51  
Job time : 41.3103 secs

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GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: November 16, 2004, 17:12:10 ; Search time 202.095 Seconds  
(without alignments)  
337.259 Million cell updates/sec

Title: US-10-036-444-2

Perfect score: 1020

Sequence: 1 MAWMLLLILVHPGSCALW.....GTHCHSSDGRGVPEPRCP 190

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 200273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A Geneseq\_23Sep04:\*

1: geneseqp1980s:\*

2: geneseqp1990s:\*

3: geneseqp2000s:\*

4: geneseqp2001s:\*

5: geneseqp2002s:\*

6: geneseqp2003as:\*

7: geneseqp2003bs:\*

8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1020	100.0	190	AAE02769	Aae02769 Human Nkp
2	1020	100.0	190	ADO19810	Ado19810 Human Nkp
3	1020	100.0	190	ADQ30923	Adq30923 Human Nkp
4	1018	99.8	190	Aay06401	Aay06401 Human B-C
5	876	85.9	201	AAy06403	AAy06403 Human B-C
6	859	84.2	177	AAy06402	AAy06402 Human B-C
7	713	69.9	135	AAE19109	AAE19109 Human Nkp
8	713	69.9	369	AAE19110	AAE19110 Human Nkp
9	632	62.0	120	AAE02771	AAE02771 Human Nkp
10	632	62.0	120	ADQ30924	Adq30924 Human Nkp
11	608.5	59.7	382	ADP48750	Adp48750 Human Nkp
12	204	20.0	33	AAE02773	AAE02773 Human Nkp
13	204	20.0	33	ADQ30926	Adq30926 Human Nkp
14	123.5	12.1	246	AAE02073	AAE02073 Human lun
15	119.5	11.7	232	ABU08020	Abu08020 Monoclonal
16	119.5	11.7	232	ADP55784	Adp55784 Human ant
17	119.5	11.7	232	ADJ92520	Adj92520 Human SQJ
18	118.5	11.6	139	AAU75565	Aau75565 Murine T
19	118.5	11.6	212	AAE0134	AAE0134 CTLA4 rec
20	118.5	11.6	212	AAE0134	AAE0134 CTLA4 rec
21	118.5	11.6	212	AAE0134	AAE0134 CTLA4 rec
22	118.5	11.6	212	AAE0134	AAE0134 CTLA4 rec
23	118.5	11.6	212	AAE0134	AAE0134 CTLA4 rec
24	118.5	11.6	212	AAE0134	AAE0134 CTLA4 rec
25	118.5	11.6	212	AAE0134	AAE0134 CTLA4 rec

26	118.5	11.6	212	6	ABP56715	Abp56715 Human CTL
27	118.5	11.6	212	7	ADD89013	Add89013 CTLA4 rec
28	116.5	11.4	212	5	AAU75126	Aau75126 Human CTL
29	116	11.4	211	2	AAW87560	Aaw87560 Human CTL
30	115.5	11.3	212	5	AAU75127	Aau75127 Human CTL
31	115.5	11.3	212	5	AAU75131	Aau75131 Human CTL
32	115.5	11.3	212	5	AAU75130	Aau75130 Human CTL
33	114.5	11.2	212	5	AAU75133	Aau75133 Human CTL
34	112	11.0	222	6	ABP59948	Abp59948 Human CTL
35	112	11.0	223	3	AAU75129	Aau75129 Human CTL
36	112	11.0	223	5	AAU74509	Aau74509 Human cyt
37	112	11.0	223	5	AAU74508	Aau74508 Human cyt
38	112	11.0	223	8	ADP12469	Adp12469 Protein e
39	112	11.0	235	4	AAU64474	Aau64474 Human typ
40	112	11.0	700	8	ADN14450	Adn14450 Mouse dop
41	111.5	10.9	212	2	AAE31040	Aae31040 Human CTL
42	111.5	10.9	212	5	AAU75129	Aau75129 Human CTL
43	111.5	10.9	226	2	AAE24112	Aae24112 Human mb-
44	111.5	10.9	226	3	AAU52553	Aau52553 Human MB-
45	111.5	10.9	226	6	ABG74347	Abg74347 Human Iga

## ALIGNMENTS

RESULT 1

AAE02769

ID AAE02769 standard; protein; 190 AA.

AC AAE02769;

XX 06-AUG-2001 (first entry)

DT Human Nkp30 receptor.

DE Human Nkp30 receptor.

XX Human; Nkp30 receptor; natural killer cell; cytostatic; antimicrobial;

KW melanoma; hepatocarcinoma; lung adenocarcinoma; viral infection; tumour;

KW immunosuppressant; antiviral; drug; grafting enhancement; leukaemia;

XX therapy.

OS Homo sapiens.

XX Location/Qualifiers

EH Key

FT Peptide

FT /label= Signal\_peptide

FT Protein

FT /label= Mature\_Nkp30\_receptor\_protein

FT Region

FT /label= Extracellular\_region

FT /note= "Forms an immunoglobulin (Ig) V-like domain"

FT Modified-site

FT /note= "N-glycosylation site"

FT Modified-site

FT /note= "N-glycosylation site"

FT Region

FT /label= Transmembrane\_region

FT Region

FT /label= Intracellular\_region

FT WO200136630-A2.

PN 25-MAY-2001.

PD 15-NOV-2000; 2000WO-EP011697.

PP 15-NOV-1999; 99CA-02288307.

XX 15-NOV-1999; 99US-00440514.

PR (INNA-) INNATE PHARMA SAS.

XX (UYGE-) UNIV GENOVA.

PA Moretta A, Bottino C, Biassoni R;

PI

XX

DR WPI; 2001-329221/34.  
 XX N-PSDB; AAD06564.  
 PT Novel compound, useful for detection and/or quantifying the presence of  
 PT NK cells, comprises the amino acid sequences of the Nkp30 molecule.  
 XX  
 XX Claim 1; Fig 7B; 83pp; English.  
 XX  
 CC The invention relates to human Nkp30 receptor and its corresponding cDNA  
 CC molecule which is involved in natural cytotoxicity mediated by natural  
 CC killer (NK) cells and antibodies that identify the same. Nkp30 receptor  
 CC is a member of immunoglobulin super family (Ig-SF). Nkp30 is selectively  
 CC expressed on the surface of human mature NK cells. Nkp30 and its cDNA are  
 CC useful for detecting and/or quantifying the presence of NK cells in a  
 CC biological sample. The invention also provide kits for detecting and/or  
 CC quantifying the presence of NK cells, for the selective removal of NK  
 CC cells from a biological sample, for the positive and selective  
 CC purification of NK cells from a biological sample and for the in vitro  
 CC stimulation of NK cell cytotoxicity. The invention further provides a  
 CC pharmaceutical composition which is used as a drug for grafting  
 CC enhancement, graft versus host (GvH) inhibition, stimulation of graft  
 CC versus tumour (GvT) and especially graft versus leukaemia (GvL), and for  
 CC the prevention, palliation and/or therapy of solid or liquid tumours,  
 CC such as melanoma, hepatocarcinoma and lung adenocarcinoma, and/or  
 CC microorganism, notably viral infection. Nkp30 antibodies are useful for  
 CC identifying Nkp30 natural ligands and allow assessment of the level of  
 CC surface Nkp30 ligand expressed on an NK-susceptible target cell and the  
 CC comparison of this level to the standard physiological one. Hence Nkp30  
 CC antibodies are useful in the diagnosis of tumours or of infection. The  
 CC present sequence is human Nkp30 receptor  
 XX  
 SQ Sequence 190 AA;  
 Query Match 100.0%; Score 1020; DB 4; Length 190;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-92;  
 Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAMWLLILIMVHPGSCALWVSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTFRDEV 60  
 DB 1 MAMWLLILIMVHPGSCALWVSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTFRDEV 60  
 QY 61 VPGKEVNGTPEFGRGLAPLASSRFLDHOAELHIRDVGRGHDSIYVCRVEVLGLGVGTG 120  
 DB 61 VPGKEVNGTPEFGRGLAPLASSRFLDHOAELHIRDVGRGHDSIYVCRVEVLGLGVGTG 120  
 QY 121 NGTRLVVEKEHPQLGAGTGVLLLRAGFYAVSFSLVAVGSTVYVYQKCHCHMGTHCHSSDGP 180  
 DB 121 NGTRLVVEKEHPQLGAGTGVLLLRAGFYAVSFSLVAVGSTVYVYQKCHCHMGTHCHSSDGP 180  
 QY 181 RGVIPERPCP 190  
 DB 181 RGVIPERPCP 190  
 RESULT 2  
 AD019810  
 ID AD019810 standard; protein; 190 AA.  
 AC AD019810;  
 XX  
 XX 12-AUG-2004 (first entry)  
 XX Human PRO polypeptide #367.  
 XX Human; PRO; immune related disorder; systemic lupus erythematosus;  
 KW rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;  
 KW systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;  
 KW autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;  
 KW diabetes mellitus; renal disease; demyelinating disease;  
 KW central nervous system; peripheral nervous system;  
 KW demyelinating polyneuropathy; Guillain-Barre syndrome;  
 KW chronic inflammatory demyelinating polyneuropathy.  
 XX

OS Homo sapiens.  
 XX WO2004043361-A2.  
 XX PD 27-MAY-2004.  
 XX PF 06-NOV-2003; 2003WO-US035268.  
 XX PR 08-NOV-2002; 2002US-0425235P.  
 XX PA (GETH ) GENENTECH INC.  
 XX PI Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;  
 PI Wood WI, Wu TD;  
 XX WPI; 2004-420067/39.  
 DR N-PSDB; ADO19809.  
 XX Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for  
 PT treating an immune related disorder such as systemic lupus erythematosus,  
 PT rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or  
 PT spondyloarthritis.  
 XX Claim 7; SEQ ID NO 734; 1731pp; English.  
 PS  
 XX The invention relates to human PRO polypeptides and the polynucleotides  
 CC encoding them. The polypeptides and polynucleotides are useful for  
 CC treating and diagnosing immune related disorders in mammals. The immune  
 CC related disorders include systemic lupus erythematosus, rheumatoid  
 CC arthritis, osteoarthritis, juvenile chronic arthritis, systemic  
 CC sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune  
 CC haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes  
 CC mellitus, immune-mediated renal disease, demyelinating diseases of the  
 CC central or peripheral nervous system, demyelinating polyneuropathy,  
 CC Guillain-Barre syndrome and chronic inflammatory demyelinating  
 CC polyneuropathy. This sequence represents a human PRO polypeptide of the  
 CC invention.  
 XX  
 SQ Sequence 190 AA;  
 Query Match 100.0%; Score 1020; DB 8; Length 190;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-92;  
 Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAMWLLILIMVHPGSCALWVSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTFRDEV 60  
 DB 1 MAMWLLILIMVHPGSCALWVSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTFRDEV 60  
 QY 61 VPGKEVNGTPEFGRGLAPLASSRFLDHOAELHIRDVGRGHDSIYVCRVEVLGLGVGTG 120  
 DB 61 VPGKEVNGTPEFGRGLAPLASSRFLDHOAELHIRDVGRGHDSIYVCRVEVLGLGVGTG 120  
 QY 121 NGTRLVVEKEHPQLGAGTGVLLLRAGFYAVSFSLVAVGSTVYVYQKCHCHMGTHCHSSDGP 180  
 DB 121 NGTRLVVEKEHPQLGAGTGVLLLRAGFYAVSFSLVAVGSTVYVYQKCHCHMGTHCHSSDGP 180  
 QY 181 RGVIPERPCP 190  
 DB 181 RGVIPERPCP 190  
 RESULT 3  
 ADQ30923  
 ID ADQ30923 standard; protein; 190 AA.  
 AC ADQ30923;  
 XX  
 XX 23-SEP-2004 (first entry)  
 XX Human Nkp30 polypeptide.  
 XX Natural killer cell; NK cell; Nkp30; cytostatic; antimicrobial.  
 XX

```
OS Homo sapiens.
XX Key Location/Qualifiers
FH Region 19..138
FT /label= Extracellular region
FT /notes= "Region specifically described in Claim 3"
FT Region 20..133
FT /label
FT /notes= "Immunogenic peptide specifically described in Claim 3"
FT Region 139..157
FT /label= Transmembrane region
FT /notes= "Region specifically described in Claim 3"
FT Region 158..190
FT /label= Cytoplasmic tail
FT /notes= "Region specifically described in Claim 3"
XX
XX WO2004056392-A1.
XX
XX 08-JUL-2004.
XX
XX 22-DEC-2003; 2003WO-EP014716.
XX
XX 23-DEC-2002; 2002US-0435344P.
XX (INNA-) INNATE PHARMA.
XX
XX Romagne F, Andre P;
XX
XX WPI; 2004-507595/48.
XX
XX Pharmaceutical compositions that stimulate proliferation of natural
XX killer cells useful for therapy of melanoma, chronic myeloid, and
XX leukemia, comprise an anti-natural killer cell receptor antibody and
XX interleukins.
XX
XX Claim 3; SEQ ID NO 1; 35pp; English.
XX
XX The present sequence is that of human NKp30, a 190 amino acid polypeptide
XX (about 30 kDa on SDS-PAGE) that is selectively expressed by natural
XX killer (NK) cells, and particularly by mature NK cells. Claimed
XX pharmaceutical compositions that have a stimulating effect on the
XX proliferation of NK cells comprise an antibody such as an anti-NKp30
XX antibody or anti-NKp46 antibody or its immuno-reactive fragment and a
XX cytokine selected from interleukin-2 (IL2), IL12, IL15 and IL21, the
XX antibody(ies) and cytokine(s) being administered together or separately
XX to a subject. The anti-NKp30 antibody is an isolated antibody or its
XX antigen-binding fragment which specifically binds to NKp30 or to a
XX fragment ADQ30924-ADQ30927 of NKp30. The pharmaceutical compositions,
XX when used for daily subcutaneous injection, comprising from 1 ng to 100
XX mg/kg (body weight) of antibody(ies), and lower than 1 million
XX units/square meters/day of cytokine(s), are useful for the prevention,
XX palliation and therapy of e.g. melanoma, chronic myeloid leukaemia, acute
XX myeloid leukaemia, lymphoma, multiple myeloma, hepatocarcinoma, lung
XX adenocarcinoma, neuroblastoma and for antimicrobial prevention,
XX palliation and therapy (claimed).
XX
XX Sequence 190 AA;
XX
XX Query Match 100.0%; Score 1020; DB 8; Length 190;
XX Best Local Similarity 100.0%; Pred. No. 8.3e-92;
XX Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 MAWMLLLILIMVHPGSCALWVSQPEIRTLGSSAFPLCSFNASQGLAIGSVTFRDEV 60
XX Db 1 MAWMLLLILIMVHPGSCALWVSQPEIRTLGSSAFPLCSFNASQGLAIGSVTFRDEV 60
XX
XX Qy 61 VPGKEVRNGTPEFGRGLAPLASSRFLHDHQAEHLIRVDRGHDAISIVCRVEVLGLGVGTG 120
XX Db 61 VPGKEVRNGTPEFGRGLAPLASSRFLHDHQAEHLIRVDRGHDAISIVCRVEVLGLGVGTG 120
XX
XX Qy 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAVGSTVYVYQKCHCHMGTHCHSSDGP 180
XX
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Db 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAVGSTVYVYQKCHCHMGTHCHSSDGP 180
Qy 181 RGVIPERPCP 190
Db 181 RGVIPERPCP 190
RESULT 4
AA06401
ID AAY06401 standard; protein; 190 AA.
XX
XX AAY06401;
XX
XX 20-SEP-1999 (first entry)
XX
XX Human B-cell myelin oligodendrocyte glycoprotein BMOG.
XX
XX BMOG; B-cell myelin oligodendrocyte glycoprotein; human;
XX signal transduction; immunomodulator; anti-inflammatory;
XX autoimmune disease; inflammation; gene therapy; diagnosis.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Peptide 1..12
FT /note= "leader peptide"
FT Protein 13..190
FT /note= "mature protein"
FT Modified-site 42
FT /note= "N-glycosylated"
FT Modified-site 58
FT /note= "N-glycosylated"
FT Modified-site 121
FT /note= "N-glycosylated"
FT Domain 139..162
FT /note= "transmembrane domain"
FT Peptide 166..190
FT /note= "alternatively spliced C-terminal end"
XX
XX WO9923867-A2.
XX
XX 20-MAY-1999.
XX
XX 05-NOV-1998; 98WO-US023826.
XX
XX 07-NOV-1997; 97US-0064761P.
XX (BIOJ ) BIOGEN INC.
XX
XX Browning J;
XX
XX WPI; 1999-418423/35.
XX N-PSDB; AAX59347.
XX
XX Novel B-cell myelin oligodendrocyte glycoproteins.
XX
XX Claim 2; Page 42; 43pp; English.
XX
XX This sequence represents human BMOG, a novel member of the B cell myelin
XX oligodendrocyte glycoprotein family that is expressed by germinal centre
XX B cells. 3 C-terminal splice variants (see AAY06401-03) of BMOG were
XX identified. The protein is present primarily in the spleen, in lymph
XX nodes and in germinal centre B cells. It may have immunoregulatory
XX functions, and soluble or chimeric fusion proteins of BMOG may be used to
XX regulate the immune system in autoimmune or inflammatory disease. Vectors
XX comprising BMOG, prokaryotic and eukaryotic host cells, and a method of
XX producing BMOG using these transformed host cells are also provided. BMOG
XX polypeptides can be used for modulating the immune system of a subject or
XX to inhibit signal transduction in a cell expressing BMOG by contacting it
XX with a soluble BMOG protein. The nucleic acid can be used for gene
XX therapy. The protein can also be used to target a toxin, imaging agent or
XX radionuclide to a cell expressing BMOG. (All claimed)
XX
```

SQ Sequence 190 AA;

Query Match 99.8%; Score 1018; DB 2; Length 190;  
 Best Local Similarity 99.5%; Pred. No. 1.3e-91;  
 Matches 189; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAWMLLLILIMVHFGSCALWVSQPEIRTLTGSSAFIPCSFNASQGRLAIGSVTWRDEV 60  
 DB 1 MAWMLLLILIMVHFGSCALWVSQPEIRTLTGSSAFIPCSFNASQGRLAIGSVTWRDEV 60

QY 61 VPGKEVRNGTPEFRGRPLAPLASSRFLHDHQAELHIRDVRGHDAIYVCRVEVLGLGVGTG 120  
 DB 61 VPGKEVRNGTPEFRGRPLAPLASSRFLHDHQAELHIRDVRGHDAIYVCRVEVLGLGVGTG 120

QY 121 NGTRLVWEKEHPQAGTIVLLLRAGFYAVSFLSVAGSTVYVYQKCHMGTHCHSSDGP 180  
 DB 121 NGTRLVWEKEHPQAGTIVLLLRAGFYAVSFLSVAGSTVYVYQKCHMGTHCHSSDGP 180

QY 181 RGVIPERCP 190  
 DB 181 RGVIPERCP 190

RESULT 5  
 AAY06403  
 ID AAY06403 standard; protein; 201 AA.  
 XX AC AAY06403;  
 XX DT 20-SEP-1999 (first entry)  
 XX DE Human B-cell myelin oligodendrocyte glycoprotein BMOG.  
 XX KW BMOG; B-cell myelin oligodendrocyte glycoprotein; human;  
 XX KW signal transduction; immunomodulator; antiinflammatory;  
 XX KW autoimmune disease; inflammation; gene therapy; diagnosis.  
 XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 FT Peptide 1..12  
 FT Protein 13..201  
 FT Modified-site 42  
 FT Modified-site 68  
 FT Modified-site 121  
 FT Domain 139..162  
 FT Peptide 166..201  
 FT /note= "alternatively spliced C-terminal end"  
 XX WO9923867-A2.  
 XX PD 20-MAY-1999.  
 XX PF 05-NOV-1998; 98WO-US023826.  
 XX PR 07-NOV-1997; 97US-0064761P.  
 XX PA (BIOJ) BIOGEN INC.  
 XX PI Browning J;  
 XX DR WFI; 1999-418423/35.  
 XX DR N-PSDS; AAX59349.  
 XX PT Novel B-cell myelin oligodendrocyte glycoproteins.  
 XX PS Claim 2; Page 43; 43pp; English.

XX This sequence represents human BMOG, a novel member of the B cell myelin oligodendrocyte glycoprotein family that is expressed by germinal centre B cells. 3 C-terminal splice variants (see AAY06401-03) of BMOG were identified. The protein is present primarily in the spleen, in lymph nodes and in germinal centre B cells. It may have immunoregulatory functions, and soluble or chimeric fusion proteins of BMOG may be used to regulate the immune system in autoimmune or inflammatory disease. Vectors comprising BMOG, prokaryotic and eukaryotic host cells, and a method of producing BMOG using these transformed host cells are also provided. BMOG polypeptides can be used for modulating the immune system of a subject or to inhibit signal transduction in a cell expressing BMOG by contacting it with a soluble BMOG protein. The nucleic acid can be used for gene therapy. The protein can also be used to target a toxin, imaging agent or radionuclide to a cell expressing BMOG. (All claimed)

XX Sequence 201 AA;  
 Query Match 85.9%; Score 876; DB 2; Length 201;  
 Best Local Similarity 89.2%; Pred. No. 1.2e-77;  
 Matches 173; Conservative 2; Mismatches 7; Indels 12; Gaps 2;

QY 1 MAWMLLLILIMVHFGSCALWVSQPEIRTLTGSSAFIPCSFNASQGRLAIGSVTWRDEV 60  
 DB 1 MAWMLLLILIMVHFGSCALWVSQPEIRTLTGSSAFIPCSFNASQGRLAIGSVTWRDEV 60

QY 61 VPGKEVRNGTPEFRGRPLAPLASSRFLHDHQAELHIRDVRGHDAIYVCRVEVLGLGVGTG 120  
 DB 61 VPGKEVRNGTPEFRGRPLAPLASSRFLHDHQAELHIRDVRGHDAIYVCRVEVLGLGVGTG 120

QY 121 NGTRLVWEKEHPQAGTIVLLLRAGFYAVSFLSVAGSTVYVYQKCHMGTHCHSSDGP 180  
 DB 121 NGTRLVWEKEHPQAGTIVLLLRAGFYAVSFLSVAGSTVYVYQKCHMGTHCHSSDGP 180

QY 181 R---GVIPERCP 190  
 DB 173 RQQLPAVVPAFLPP 186

RESULT 6  
 AAY06402  
 ID AAY06402 standard; protein; 177 AA.  
 XX AC AAY06402;  
 XX DT 20-SEP-1999 (first entry)  
 XX DE Human B-cell myelin oligodendrocyte glycoprotein BMOG.  
 XX KW BMOG; B-cell myelin oligodendrocyte glycoprotein; human;  
 XX KW signal transduction; immunomodulator; antiinflammatory;  
 XX KW autoimmune disease; inflammation; gene therapy; diagnosis.  
 XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 FT Peptide 1..12  
 FT Protein 13..177  
 FT Modified-site 42  
 FT Modified-site 68  
 FT Modified-site 121  
 FT Domain 139..162  
 FT Peptide 166..177  
 FT /note= "alternatively spliced C-terminal end"  
 XX WO9923867-A2.  
 XX PD 20-MAY-1999.  
 XX PF 05-NOV-1998; 98WO-US023826.  
 XX PR 07-NOV-1997; 97US-0064761P.  
 XX PA (BIOJ) BIOGEN INC.  
 XX PI Browning J;  
 XX DR WFI; 1999-418423/35.  
 XX DR N-PSDS; AAX59349.  
 XX PT Novel B-cell myelin oligodendrocyte glycoproteins.  
 XX PS Claim 2; Page 43; 43pp; English.



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XX PN WO200208287-A2.
XX PD 31-JAN-2002.
XX PF 19-JUL-2001; 2001WO-IL000664.
XX PR 20-JUL-2000; 2000IL-00137419.
XX PA (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
XX PA (UYNE ) UNIV BEN-GURION NEGEV.
XX PI Mandelboim O, Porgador A;
XX WI; 2002-195870/25.
XX DR N-PSDB; AAD30467.
XX PS
XX CC The invention relates to compositions and methods for the treatment and
XX CC detection of a variety of viral infections, by using complex agents
XX CC comprising the natural killer (NK) cells activating proteins, Nkp46 and
XX CC Nkp44 and functional fragments thereof, linked to therapeutic or imaging
XX CC agents. The complex is useful for treating pathologies associated with
XX CC viral infections (e.g. infections caused by influenza virus, HIV, Epstein
XX CC -Barr virus, cytomegalovirus, vaccinia virus, ECV, MVM or herpes virus)
XX CC and cancer (e.g. carcinomas, melanomas, lymphomas and sarcomas), and for
XX CC the imaging and monitoring of cancer. The complex may also be used to
XX CC detect the presence of abnormal cells in a sample. The antibodies can be
XX CC used to qualitatively or quantitatively detect the ligand for the
XX CC complex. The present sequence is human Nkp30- immunoglobulin G (IgG) Fc
XX CC region fusion protein. (Updated on 29-AUG-2003 to standardise OS field)
XX PS
XX CC Sequence 369 AA;
XX CC
XX CC Query Match 69.9%; Score 713; DB 5; Length 369;
XX CC Best Local Similarity 100.0%; Pred. No. 2.8e-61;
XX CC Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX CC
QY 1 MAMWLLILLIMVHPGSCALWVSOPPEIRTLGSSAFPLPCSFNASQGRLAIGSVTWFREDEV 60
DB 1 MAMWLLILLIMVHPGSCALWVSOPPEIRTLGSSAFPLPCSFNASQGRLAIGSVTWFREDEV 60
QY 61 VPKQEVNRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVLGLGVGTG 120
DB 61 VPKQEVNRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVLGLGVGTG 120
QY 121 NGRLVVEKEHPOLG 135
DB 121 NGRLVVEKEHPOLG 135
RESULT 9
AAE02771
ID AAE02771 standard; protein; 120 AA.
XX AC AAE02771;
XX DT 06-AUG-2001 (first entry)
XX DE Human Nkp30 receptor extracellular region sequence.
XX KW Human; Nkp30 receptor; natural killer cell; cytostatic; antimicrobial;
XX KW melanoma; hepatocarcinoma; lung adenocarcinoma; viral infection; tumour;
XX KW immunosuppressant; antiviral; drug; grafting enhancement; leukaemia;
XX KW therapy; extracellular region.
XX OS Homo sapiens.

```

```

XX PN WO200136630-A2.
XX PD 25-MAY-2001.
XX PF 15-NOV-2000; 2000WO-EP011697.
XX PR 15-NOV-1995; 99CA-02288307.
XX PR 15-NOV-1995; 99US-00440514.
XX PA (INNA-) INVATE PHARMA SAS.
XX PA (UYNE-) UNIV GENOVA.
XX PI Moretta A, Bottino C, Biassoni R;
XX WI; 2001-329221/34.
XX DR
XX PS
XX CC Novel compound, useful for detection and/or quantifying the presence of
XX CC NK cells, comprises the amino acid sequences of the Nkp30 molecule.
XX CC
XX CC Claim 1; Fig 7B; 83pp; English.
XX CC
XX CC The invention relates to human Nkp30 receptor and its corresponding cDNA
XX CC molecule which is involved in natural cytotoxicity mediated by natural
XX CC killer (NK) cells and antibodies that identify the same. Nkp30 receptor
XX CC is a member of immunoglobulin super family (Ig-SF). Nkp30 is selectively
XX CC expressed on the surface of human mature NK cells. Nkp30 and its cDNA are
XX CC useful for detecting and/or quantifying the presence of NK cells in a
XX CC biological sample. The invention also provide kits for detecting and/or
XX CC quantifying the presence of NK cells, for the selective removal of NK
XX CC cells from a biological sample, for the positive and selective
XX CC purification of NK cells from a biological sample and for the in vitro
XX CC stimulation of NK cell cytotoxicity. The invention further provides a
XX CC pharmaceutical composition which is used as a drug for grafting
XX CC enhancement, graft versus host (GvH) inhibition, stimulation of graft
XX CC versus tumour (GvT) and especially graft versus leukaemia (GvL), and for
XX CC the prevention, palliation and/or therapy of solid or liquid tumours,
XX CC such as melanoma, hepatocarcinoma and lung adenocarcinoma, and/or
XX CC microorganism, notably viral infection. Nkp30 antibodies are useful for
XX CC identifying Nkp30 natural ligands and allow assessment of the level of
XX CC surface Nkp30 ligand expressed on an NK-susceptible target cell and the
XX CC comparison of this level to the standard physiological one. Hence Nkp30
XX CC antibodies are useful in the diagnosis of tumours or of infection. The
XX CC present sequence is the extracellular region of human Nkp30 receptor
XX CC
XX CC Sequence 120 AA;
XX CC
XX CC Query Match 62.0%; Score 632; DB 4; Length 120;
XX CC Best Local Similarity 100.0%; Pred. No. 5.9e-54;
XX CC Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX CC
QY 19 LWSQPPPEIRTLGSSAFPLPCSFNASQGRLAIGSVTWFREDEVVPGKEVRNGTPEFRGLA 78
DB 1 LWSQPPPEIRTLGSSAFPLPCSFNASQGRLAIGSVTWFREDEVVPGKEVRNGTPEFRGLA 60
QY 79 PLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVLGLGVGTGNGTGLVVEKEHPOLGAGT 138
DB 61 PLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVLGLGVGTGNGTGLVVEKEHPOLGAGT 120
RESULT 10
ADQ30924
ID ADQ30924 standard; protein; 120 AA.
XX AC ADQ30924;
XX DT 23-SEP-2004 (first entry)
XX DE Human Nkp30 extracellular region.
XX KW Natural killer cell; NK cell; Nkp30; cytostatic; antimicrobial.
XX OS Homo sapiens.

```

XX PN WO2004056392-A1.  
 XX PD 08-JUL-2004.  
 XX PF 22-DEC-2003; 2003WO-EP014716.  
 XX PR 23-DEC-2002; 2002US-0435344P.  
 XX PA (INNA-) INNATE PHARMA.  
 XX PI Romagne F, Andre P;  
 XX DR WPI; 2004-507595/48.  
 XX XX  
 XX PT Pharmaceutical compositions that stimulate proliferation of natural  
 PT killer cells useful for therapy of melanoma, chronic myeloid, and  
 PT leukemia, comprise an anti-natural killer cell receptor antibody and  
 PT interleukins.  
 XX PS Claim 3; SEQ ID NO 2; 35pp; English.  
 XX XX  
 CC The present sequence is that of the extracellular region of human NKp30  
 CC ADQ30923, a 190 amino acid polypeptide that is selectively expressed by  
 CC natural killer (NK) cells, and particularly by mature NK cells. Claimed  
 CC pharmaceutical compositions that have a stimulating effect on the  
 CC proliferation of NK cells comprise an antibody such as an anti-NKp30  
 CC antibody or anti-NKp46 antibody or its immuno-reactive fragment and a  
 CC cytokine selected from interleukin-2 (IL2), IL12, IL15 and IL21, the  
 CC antibody(ies) and cytokine(s) being administered together or separately  
 CC to a subject. The anti-NKp30 antibody is an isolated antibody or its  
 CC antigen-binding fragment which specifically binds to NKp30 or to a  
 CC fragment, including the extracellular region, of NKp30. The  
 CC pharmaceutical compositions, when used for daily subcutaneous injection,  
 CC comprising from 1 ng to 100 mg/kg (body weight) of antibody(ies), and  
 CC lower than 1 million units/square meters/day of cytokine(s), are useful  
 CC for the prevention, palliation and therapy of e.g. melanoma, chronic  
 CC myeloid leukaemia, acute myeloid leukaemia, lymphoma, multiple myeloma,  
 CC hepatocarcinoma, lung adenocarcinoma, neuroblastoma and for antimicrobial  
 CC prevention, palliation and therapy (claimed).  
 XX SQ Sequence 120 AA;  
 XX XX  
 Query Match 62.0%; Score 632; DB 8; Length 120;  
 Best Local Similarity 100.0%; Pred. No. 5,9e-54;  
 Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 19 LWSQPPPIRTLEGSSAFPCSFNQSQRGAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 78  
 Db 1 LWSQPPPIRTLEGSSAFPCSFNQSQRGAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 60  
 Qy 79 PLASSRFLHDHQAELHVRDVRGHDAIYVCRVEVLGVTGTGTRLVWEKEHPQLGAGT 138  
 Db 61 PLASSRFLHDHQAELHVRDVRGHDAIYVCRVEVLGVTGTGTRLVWEKEHPQLGAGT 120  
 RESULT 11  
 ADP48750  
 ID ADP48750 standard; protein; 382 AA.  
 XX AC ADP48750;  
 XX XX  
 XX 09-SEP-2004 (first entry)  
 XX XX  
 XX Human NKp30-Fc conjugate protein SEQ ID NO:12.  
 XX XX  
 KW polypeptide conjugate; target recognition; natural killer cell receptor;  
 KW cytostatic; gene therapy; neoplastic disease; tumour; carcinoma;  
 KW squamous cell carcinoma; adenocarcinoma; small cell carcinoma; melanoma;  
 KW glioma; neuroblastoma; B cell lymphoma; T cell lymphoma; leukaemia;  
 KW human; natural killer cytotoxicity receptor conjugate;  
 KW NKp30-Fc conjugate.  
 XX XX

OS Homo sapiens.  
 XX Key  
 XX FT Peptide  
 XX FT Protein  
 XX FT /label= signal  
 XX FT /note= "NKp30-Fc conjugate"  
 XX FT Misc-difference 26..31  
 XX FT /note= "Kpni site"  
 XX FT Region 32..148  
 XX FT /label= NKp30  
 XX FT Region 149..382  
 XX FT /label= Fc  
 XX XX  
 PN WO2004053054-A2.  
 XX XX  
 XX PD 24-JUN-2004.  
 XX XX  
 XX PF 09-DEC-2003; 2003WO-IL001040.  
 XX XX  
 XX PR 09-DEC-2002; 2002US-0431728P.  
 XX XX  
 XX (NATS-) NATSPEARS LTD.  
 XX PA Mandelboim O, Porgador A;  
 XX PI  
 XX DR WPI; 2004-468830/44.  
 XX DR N-PSDB; ADP48757.  
 XX XX  
 XX New polypeptide conjugate comprising a target recognition segment  
 XX comprising a Natural Killer cell receptor consisting of NKp30, useful in  
 XX preparing a composition for treating a neoplastic disease.  
 XX PS Claim 5; SEQ ID NO 4; 66pp; English.  
 XX XX  
 CC The present invention describes a polypeptide conjugate comprising: (a) a  
 CC target recognition segment comprising a natural killer cell receptor  
 CC (NCR) or its fragment consisting of NKp30 or its fragment that binds to a  
 CC cellular ligand expressed on the surface of a target tumour cell; and (b)  
 CC a second segment comprising an active agent capable of exerting a  
 CC cytotoxic effect on the target cell. Also described: (1) an isolated  
 CC polynucleotide encoding the polypeptide conjugate; (2) a vector  
 CC comprising the polynucleotide; (3) a host cell comprising the vector and  
 CC capable of expressing the polypeptide conjugate; (4) a pharmaceutical  
 CC composition comprising the polypeptide conjugate and a carrier,  
 CC stabiliser or diluent; (5) treating a neoplastic disease in a subject;  
 CC (6) inhibiting the growth of a tumour in a subject; and (7) delivering a  
 CC cytotoxic substance to a target tumour cell in a subject. The polypeptide  
 CC conjugate has cytostatic activity, and can be used in gene therapy. The  
 CC polypeptide conjugate is useful in preparing a composition for treating a  
 CC neoplastic disease associated with a solid tumour or a non-solid tumour,  
 CC e.g., carcinoma, squamous cell carcinomas, adenocarcinomas, small cell  
 CC carcinomas, melanomas, gliomas, neuroblastomas, B cell lymphoma, T cell  
 CC lymphoma or leukaemia. The present sequence represents a human natural  
 CC killer cytotoxicity receptor conjugate, designated NKp30-Fc conjugate,  
 CC which is used in the exemplification of the present invention.  
 XX SQ Sequence 382 AA;  
 XX XX  
 Query Match 59.7%; Score 608.5; DB 8; Length 382;  
 Best Local Similarity 85.8%; Pred. No. 5,3e-51;  
 Matches 121; Conservative 5; Mismatches 6; Indels 9; Gaps 2;  
 Qy 1 MAWMLLLILIMVHPGSC-----ALWVSQPPPIRTLEGSSAFPCSFNQSQRGAIGSVT 54  
 Db 11 LATLVLLGLMLV---ASCLGRIRVPLWVSQPLEIRTLGSSAFPCSFNQSQRGAIGSVT 67  
 Qy 55 WFRDEVVPGKEVRNGTPEFRGLAFLASSRFLHDHQAELHVRDVRGHDAIYVCRVEVLG 114  
 Db 68 WFRDEVVPGKEVRNGTPEFRGLAFLASSRFLHDHQAELHVRDVRGHDAIYVCRVEVLG 127  
 Qy 115 LGVGTGTGTGTRLVWEKEHPQLG 135





```
DT 18-JUN-2002 (first entry)
XX
XX Human lung specific gene (LSG) protein #11.
XX
XX Human; lung specific gene; LSG; lung embryonic development; cytostatic;
XX lung cancer; vaccine; gene therapy; non-cancerous lung disease; tumour.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Region 189..204
XX /note= "Antigenic epitope"
XX
XX WO200208278-A2.
XX
XX 31-JAN-2002.
XX
XX 20-JUL-2001; 2001WO-US022949.
XX
XX 21-JUL-2000; 2000US-0219834P.
XX
XX (DIAD-) DIADEXUS INC.
XX
XX Macina RA, Nair M, Chen S;
XX
XX WPI; 2002-268964/31.
XX
XX Novel lung specific gene useful for identifying, diagnosing, monitoring,
XX staging, imaging and treating lung cancer and non-cancerous disease
XX states in lung, for gene therapy, and for identifying lung tissue.
XX
XX Claim 2; Page 178-179; 197pp; English.
XX
XX The present invention relates to lung specific genes (LSG) and their
XX corresponding polypeptides. LSG is useful for identifying, diagnosing,
XX monitoring, staging, imaging and treating lung cancer and non-cancerous
XX disease states in lung, identifying lung tissue, monitoring and modifying
XX lung embryonic development and differentiation, in gene therapy, as
XX hybridisation probes, to detect LSG mRNA as a marker for lung cancer, as
XX research reagents and materials for discovery of treatments and
XX diagnostics to human disease, to detect complementary polynucleotides,
XX and for chromosome identification. An antibody which binds LSG is useful
XX to detect or image localisation of LSG in a patient for detecting or
XX diagnosing a disease or condition, for preventing the onset and treatment
XX of lung cancer, to isolate or to identify clones expressing LSG
XX polypeptides, to purify LSG polypeptides, and to target tumours
XX expressing LSG. The present sequence is human LSG protein
XX
XX Sequence 246 AA;
XX
XX Query Match 12.1%; Score 123.5; DB 5; Length 246;
XX Best Local Similarity 29.2%; Pred. No. 0.0013;
XX Matches 54; Conservative 17; Mismatches 61; Indels 53; Gaps 10;
XX
XX QY 1 MAMM-LLILLIMVHPGSCALWV-SQPPEIRTELESSAFPCSFNASQGRLAIGSVTFWRD 58
XX ||| ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
XX 1 MAMAPLLTLLSLTGSQIPQLTPPSASASLGASVTLTCSVSSDYKNI---EVDWFOQ 57
XX
XX 59 EVVPGKEVR-----NGTPEFRGLAP-----LASSRFLHDHQAELHIRDVRGHDA 104
XX ||| ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
XX 58 R--FGKGRFVMRYGTGGVGFGRADIPDRFSVSGSLNRF-----LIRNIEEDES 108
XX
XX 105 IYVCRVEVLGUGVT-----GNTRLVW-----EKEHPQLGAGTVLL 142
XX ||| ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
XX 109 DYHCGTD---LGSQTSFVSWVFGGGLTKLTVLSQPKAAPSVTLFPPSSEELQANKATLVCL 165
XX
XX 143 RAGFY 147
XX
XX 166 ISDFY 170
XX
XX RESULT 15
XX ABU08020
```

```
ID ABU08020 standard; protein; 232 AA.
XX
XX AC ABU08020;
XX
XX 10-MAY-2003 (first entry)
XX
XX Monoclonal rabies virus antibody light chain, clone JB.1.
XX
XX Human; antibody; constant region; monoclonal antibody 57; Mab 57;
XX variable region; Rabies; neurological disease; infection;
XX central nervous system; rabies virus; Lyssavirus; Rhabdoviridae;
XX pathogen; vaccine; virucide; light chain.
XX
XX Homo sapiens.
XX
XX WO2003016501-A2.
XX
XX 27-FEB-2003.
XX
XX 21-AUG-2002; 2002WO-US026584.
XX
XX 21-AUG-2001; 2001US-0314023P.
XX
XX (UYOE-) UNIV JEFFERSON THOMAS.
XX
XX Hooper DC, Dietzschold B;
XX
XX WPI; 2003-278566/27.
XX
XX N-PSDB; ABX12862.
XX
XX New recombinant antibody comprising a constant region of Mab 57 linked to
XX a non-Mab 57 variable region, useful for treating an individual exposed
XX to a pathogen, e.g. rabies infection.
XX
XX Claim 1; Page 36; 38pp; English.
XX
XX The invention discloses a recombinant antibody comprising a constant
XX region of monoclonal antibody (Mab) 57 linked to a non-Mab 57 variable
XX region. Rabies is an acute, neurological disease caused by infection of
XX the central nervous system with the rabies virus, a member of the
XX Lyssavirus genus of the family Rhabdoviridae. Also disclosed are methods
XX for producing an isolated recombinant antibody by culturing a host cell,
XX containing a recombinant expression vector comprising the recombinant antibody
XX molecule encoding the antibody, and isolating the recombinant antibody
XX expressed and treating an individual exposed to a pathogen by
XX administering to the individual the recombinant antibody. The recombinant
XX antibodies are useful for preventing (vaccine) and treating an individual
XX exposed to a pathogen, e.g. rabies infection. They are also useful for
XX the qualitative and quantitative determination of the rabies virus. The
XX sequences presented are the antibody protein fragments, the nucleic acids
XX encoding them or the PCR primers used to construct the recombinant
XX expression vector
XX
XX Sequence 232 AA;
XX
XX Query Match 11.7%; Score 119.5; DB 6; Length 232;
XX Best Local Similarity 26.0%; Pred. No. 0.0029;
XX Matches 45; Conservative 25; Mismatches 64; Indels 39; Gaps 7;
XX
XX QY 1 MAMM-LLILLIMVH-PGSCALWV-SQPPEIRTELESSAFPCSFNASQGRLAIGSVTFWRD 58
XX ||| ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
XX 1 MAWTVLLGLLSHCTGTSVTSVLTQTPSVSVAPGKTARINCGNNIEYR---SVHWYQQ 56
XX
XX 59 E-----VVPGEVRNGTPE-FGRGLAPLASSRFLHDHQAELHIRDVRGHDA 109
XX ||| ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
XX 57 KSGQAPVAVIYDNSDRPSGIPERFSGSKS-----GNTATLTISRVEAGDEADYVQ 107
XX
XX 110 VEVLGLGVGTGNTRLVW-----EKEHPQLGAGTVLLRAGFY 147
XX ||| ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
XX 108 VWDISDVFVGGGTLTKLVLPQPKAAPSVTLFPPSSEELQANKATLVCLISDFY 160
XX
XX Search completed: November 16, 2004, 18:55:51
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Wed Nov 17 05:46:29 2004

us-10-036-444-2.open.rag

Page 10

Job time : 206.095 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 16, 2004, 19:14:52 ; Search time 169.841 Seconds  
(without alignments)  
395.815 Million cell updates/sec

Title: US-10-036-444-2

Perfect score: 1020

Sequence: 1 MAWMLLLILIMVHPSGSCALW.....GTHCHSSDGRGVIPRCP 190

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1568699 seqs, 353819137 residues

Total number of hits satisfying chosen parameters: 1568699

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications AA:  
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19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1020	100.0	190	13	US-10-036-444-2
2	1020	100.0	190	16	US-10-696-259-4
3	956.5	93.8	185	16	US-10-696-259-7
4	876	85.9	201	16	US-10-696-259-6
5	859	84.2	177	16	US-10-696-259-5
6	842.5	82.6	198	16	US-10-696-259-9
7	828.5	81.2	161	16	US-10-696-259-10
8	825	80.9	175	16	US-10-696-259-8
9	713	69.9	135	15	US-10-333-481-17
10	713	69.9	369	15	US-10-333-481-18
11	632	62.0	120	13	US-10-036-444-4
12	204	20.1	33	13	US-10-036-444-6
13	123.5	12.1	246	10	US-09-909-567B-49

14	119.5	11.7	232	14	US-10-225-108A-12
15	119.5	11.7	232	15	US-10-461-148-6
16	118.5	11.6	139	14	US-10-312-495-6
17	118.5	11.6	212	10	US-09-898-195A-17
18	118.5	11.6	212	14	US-10-057-288-12
19	118.5	11.6	212	14	US-10-155-514-2
20	118.5	11.6	212	15	US-10-419-008-17
21	111.5	10.9	226	13	US-10-038-107A-1
22	111.5	10.9	226	14	US-10-371-525-32
23	111.5	10.9	226	14	US-10-371-069-32
24	111.5	10.9	226	14	US-10-371-645-32
25	111.5	10.9	226	14	US-10-371-260-32
26	111.5	10.9	226	14	US-10-411-010-19
27	111	10.9	223	15	US-10-383-201-20
28	110	10.8	223	9	US-09-989-545-21
29	110	10.8	223	10	US-09-928-267-18
30	110	10.8	223	10	US-09-928-267-21
31	110	10.8	223	14	US-10-225-519-8
32	110	10.8	223	14	US-10-207-655-101
33	108.5	10.6	223	9	US-09-989-545-20
34	108.5	10.6	223	14	US-10-211-207-5
35	108.5	10.6	223	14	US-10-077-106-5
36	108.5	10.6	223	16	US-10-750-396-42
37	108.5	10.6	223	17	US-10-748-112-19
38	108.5	10.6	383	10	US-09-898-195A-11
39	108.5	10.6	383	14	US-10-057-288-6
40	108.5	10.6	383	14	US-10-155-514-10
41	108.5	10.6	383	15	US-10-419-008-11
42	108	10.6	223	13	US-10-107-828-26
43	108	10.6	223	13	US-10-107-907-26
44	108	10.6	223	13	US-10-107-868-26
45	108	10.6	223	14	US-10-301-056-26

#### ALIGNMENTS

#### RESULT 1

US-10-036-444-2  
; Sequence 2, Application US/10036444  
; Publication No. US20020142445A1  
; GENERAL INFORMATION:  
; APPLICANT: INNATE PHARMA S.A.S.  
; APPLICANT: UNIVERSITA DI GENOVA  
; TITLE OF INVENTION: "NO. US20020142445A1el triggering receptor involved in natural  
; TITLE OF INVENTION: cytotoxicity mediated by human Natural Killer cells and  
; TITLE OF INVENTION: antibodies that identify the same"  
; FILE REFERENCE: SEQ-FR-1060  
; CURRENT APPLICATION NUMBER: US/10/036,444  
; CURRENT FILING DATE: 2002-01-07  
; PRIOR APPLICATION NUMBER: 09/440,514  
; PRIOR FILING DATE: 1999-11-15  
; PRIOR APPLICATION NUMBER: 09/456,199  
; PRIOR FILING DATE: 1999-12-07  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 190  
; TYPE: PRT  
; ORGANISM: Human NK cell  
; US-10-036-444-2

Query Match 100.0%; Score 1020; DB 13; Length 190;

Best Local Similarity 100.0%; Pred. No. 3.1e-93; Mismatches 0; Indels 0; Gaps 0;

Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAWMLLLILIMVHPSGSCALWVSQPPPIRTLEGSSAFPCSFNASQGLAIGSVTFRDEV 60

Db 1 MAWMLLLILIMVHPSGSCALWVSQPPPIRTLEGSSAFPCSFNASQGLAIGSVTFRDEV 60

QY 61 VPGKEVRNGTPTFRGRGLAPLASSRLHDLHQRHLDVGRGHDASTVYVCEVVLGLGVGTG 120

Db 61 VPGKEVRNGTPTFRGRGLAPLASSRLHDLHQRHLDVGRGHDASTVYVCEVVLGLGVGTG 120

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QY 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFSLVAVGSTVYYQKCHCHMGTHCHSSDGP 180
DB 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFSLVAVGSTVYYQKCHCHMGTHCHSSDGP 180
QY 181 RGVPEPRCP 190
DB 181 RGVPEPRCP 190

RESULT 2
US-10-696-259-4
; Sequence 4, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; TITLE OF INVENTION: BROWNING, Jeffrey
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-4
Query Match 100.0%; Score 1020; DB 16; Length 190;
Best Local Similarity 100.0%; Pred. No. 3.1e-93;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAWMLLLILIMVHPGSCALWVSQPPETRTLGSSAFPLPCSFNASQGRLAIGSVTWFRDEV 60
DB 1 MAWMLLLILIMVHPGSCALWVSQPPETRTLGSSAFPLPCSFNASQGRLAIGSVTWFRDEV 60
QY 61 VPGKEVRNGTPEFRGLAPLASSRFLHDHQAEHLHIRDVRGHDASIYVCRVEVLGLGVGTG 120
DB 61 VPGKEVRNGTPEFRGLAPLASSRFLHDHQAEHLHIRDVRGHDASIYVCRVEVLGLGVGTG 120
QY 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFSLVAVGSTVYYQKCHCHMGTHCHSSDGP 180
DB 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFSLVAVGSTVYYQKCHCHMGTHCHSSDGP 180
QY 181 RGVPEPRCP 190
DB 181 RGVPEPRCP 190

RESULT 3
US-10-696-259-7
; Sequence 7, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; TITLE OF INVENTION: BROWNING, Jeffrey
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-7
Query Match 100.0%; Score 1020; DB 16; Length 190;
Best Local Similarity 100.0%; Pred. No. 3.1e-93;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAWMLLLILIMVHPGSCALWVSQPPETRTLGSSAFPLPCSFNASQGRLAIGSVTWFRDEV 60
DB 1 MAWMLLLILIMVHPGSCALWVSQPPETRTLGSSAFPLPCSFNASQGRLAIGSVTWFRDEV 60
QY 61 VPGKEVRNGTPEFRGLAPLASSRFLHDHQAEHLHIRDVRGHDASIYVCRVEVLGLGVGTG 120
DB 61 VPGKEVRNGTPEFRGLAPLASSRFLHDHQAEHLHIRDVRGHDASIYVCRVEVLGLGVGTG 120
QY 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFSLVAVGSTVYYQKCHCHMGTHCHSSDGP 180
DB 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFSLVAVGSTVYYQKCHCHMGTHCHSSDGP 180
QY 181 RGVPEPRCP 190
DB 181 RGVPEPRCP 190

RESULT 4
US-10-696-259-6
; Sequence 6, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-6
Query Match 85.9%; Score 876; DB 16; Length 201;
Best Local Similarity 89.2%; Pred. No. 7.2e-79;
Matches 173; Conservative 2; Mismatches 7; Indels 12; Gaps 2;
QY 1 MAWMLLLILIMVHPGSCALWVSQPPETRTLGSSAFPLPCSFNASQGRLAIGSVTWFRDEV 60
DB 1 MAWMLLLILIMVHPGSCALWVSQPPETRTLGSSAFPLPCSFNASQGRLAIGSVTWFRDEV 60
QY 61 VPGKEVRNGTPEFRGLAPLASSRFLHDHQAEHLHIRDVRGHDASIYVCRVEVLGLGVGTG 120
DB 61 VPGKEVRNGTPEFRGLAPLASSRFLHDHQAEHLHIRDVRGHDASIYVCRVEVLGLGVGTG 120
QY 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFSLVAVGSTVYYQKCHCHMGTHCHSSDGP 180
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Db      121  NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFSLVAVGSTVYYQK-----CLTWKGP 172
QY      181  R----GVIPERCP 190
Db      173  RRQLFAVVPAPLPP 186

RESULT 5
US-10-696-259-5
; Sequence 5, Application US/10696259
; Publication No. US200401102181
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-5

Query Match      84.2%; Score 859; DB 16; Length 177;
Best Local Similarity 100.0%; Pred. No. 3e-77;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MAWMLLLILIMVHPGSCALWVSQPEIRTLGSSAFLPCSFNASQGLAIGSVTWERDEV 60
Db      1  MAWMLLLILIMVHPGSCALWVSQPEIRTLGSSAFLPCSFNASQGLAIGSVTWERDEV 60
QY      61  VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTG 120
Db      61  VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTG 120
QY      121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFSLVAVGSTVYYQK 165
Db      121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFSLVAVGSTVYYQK 165

RESULT 6
US-10-696-259-9
; Sequence 9, Application US/10696259
; Publication No. US200401102181
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-9

Query Match      81.2%; Score 828.5; DB 16; Length 161;
Best Local Similarity 99.4%; Pred. No. 2.9e-74;
Matches 161; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY      1  MAWMLLLILIMVHPGSCALWVSQPEIRTLGSSAFLPCSFNASQGLAIGSVTWERDEV 60
Db      1  MAWMLLLILIMVHPGSCALWVSQPEIRTLGSSAFLPCSFNASQGLAIGSVTWERDEV 60
QY      61  VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTG 120
Db      61  VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTG 119
QY      121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFSLVAVGSTVYY 162
Db      120 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFSLVAVGSTVYY 161

RESULT 8
US-10-696-259-8
```

```
; SEQ ID NO 9
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-9

Query Match      82.6%; Score 842.5; DB 16; Length 198;
Best Local Similarity 88.1%; Pred. No. 1.5e-75;
Matches 170; Conservative 2; Mismatches 8; Indels 13; Gaps 4;

QY      1  MAWMLLLILIMVHPGSCALWVSQPEIRTLGSSAFLPCSFNASQGLAIGSVTWERDEV 60
Db      1  MAWMLLLILIMVHPGSCALWVSQPEIRTLGSSAFLPCSFNASQGLAIGSVTWERDEV 59
QY      61  VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTG 120
Db      60  VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTG 118
QY      121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFSLVAVGSTVYYQKCHHGMTHCHSDGP 180
Db      119 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFSLVAVGSTVYYHGK-----CLTWKGP 170
QY      181  R---GVIPERCP 190
Db      171  RRLPAVVPAPLPP 183

RESULT 7
US-10-696-259-10
; Sequence 10, Application US/10696259
; Publication No. US200401102181
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-10

Query Match      81.2%; Score 828.5; DB 16; Length 161;
Best Local Similarity 99.4%; Pred. No. 2.9e-74;
Matches 161; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY      1  MAWMLLLILIMVHPGSCALWVSQPEIRTLGSSAFLPCSFNASQGLAIGSVTWERDEV 60
Db      1  MAWMLLLILIMVHPGSCALWVSQPEIRTLGSSAFLPCSFNASQGLAIGSVTWERDEV 60
QY      61  VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTG 120
Db      61  VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTG 119
QY      121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFSLVAVGSTVYY 162
Db      120 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFSLVAVGSTVYY 161

RESULT 8
US-10-696-259-8
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; Sequence 8, Application US/10696259  
; Publication No. US20040110218A1  
; GENERAL INFORMATION:  
; APPLICANT: BIOGEN, INC  
; APPLICANT: BROWNING, Jeffrey  
; TITLE OF INVENTION: BMG, A Novel Protein Member of the  
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for  
; TITLE OF INVENTION: Immunomodulatory Purposes  
; FILE REFERENCE: A041 US  
; CURRENT APPLICATION NUMBER: US/10/696,259  
; PRIOR FILING DATE: 2003-10-28  
; PRIOR APPLICATION NUMBER: US/09/560,855A  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: PCT/US98/23826  
; PRIOR FILING DATE: 1998-11-05  
; PRIOR APPLICATION NUMBER: 60/064761  
; PRIOR FILING DATE: 1997-11-07  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 175  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-696-259-8

Query Match 80.9%; Score 825; DB 16; Length 175;  
Best Local Similarity 98.2%; Pred. No. 7.2e-74;  
Matches 162; Conservative 0; Mismatches 1; Indels 2; Gaps 2;  
QY 1 MAMLLILIMVHPGSCALWVSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWFRDEV 60  
DB 1 MAMLLILIMVHPGSCALWVSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWFRDEV 59  
QY 61 VPGKEVNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVLGLGVGTG 120  
DB 60 VPGKEVNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVLGLGVGTG 118  
QY 121 NGTRLVVEKEHPOLGAGTVLLLRAGFVAVSFLSVAGSTVYVYGGK 165  
DB 119 NGTRLVVEKEHPOLGAGTVLLLRAGFVAVSFLSVAGSVYVYHGK 163

RESULT 9  
US-10-333-481-17  
; Sequence 17, Application US/10333481  
; Publication No. US20040072256A1  
; GENERAL INFORMATION:  
; APPLICANT: Ofel Mandelboim  
; APPLICANT: Angel Porcador  
; TITLE OF INVENTION: NK CELLS ACTIVATING RECEPTORS AND THEIR THERAPEUTIC AND DIAGNOSIT  
; FILE REFERENCE: 68657  
; CURRENT APPLICATION NUMBER: US/10/333,481  
; CURRENT FILING DATE: 2003-08-04  
; PRIOR APPLICATION NUMBER: PCT/IL01/00664  
; PRIOR FILING DATE: 2001-07-19  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 17  
; LENGTH: 135  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-333-481-17

Query Match 69.9%; Score 713; DB 15; Length 135;  
Best Local Similarity 100.0%; Pred. No. 7.3e-63;  
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAMLLILIMVHPGSCALWVSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWFRDEV 60  
DB 1 MAMLLILIMVHPGSCALWVSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWFRDEV 60  
QY 61 VPGKEVNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVLGLGVGTG 120

Db 61 VPGKEVNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVLGLGVGTG 120  
QY 121 NGTRLVVEKEHPOLG 135  
DB 121 NGTRLVVEKEHPOLG 135

RESULT 10  
US-10-333-481-18  
; Sequence 18, Application US/10333481  
; Publication No. US20040072256A1  
; GENERAL INFORMATION:  
; APPLICANT: Ofel Mandelboim  
; APPLICANT: Angel Porcador  
; TITLE OF INVENTION: NK CELLS ACTIVATING RECEPTORS AND THEIR THERAPEUTIC AND DIAGNOSIT  
; FILE REFERENCE: 68657  
; CURRENT APPLICATION NUMBER: US/10/333,481  
; CURRENT FILING DATE: 2003-08-04  
; PRIOR APPLICATION NUMBER: PCT/IL01/00664  
; PRIOR FILING DATE: 2001-07-19  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 369  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-333-481-18

Query Match 69.9%; Score 713; DB 15; Length 369;  
Best Local Similarity 100.0%; Pred. No. 2.6e-82;  
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAMLLILIMVHPGSCALWVSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWFRDEV 60  
DB 1 MAMLLILIMVHPGSCALWVSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWFRDEV 60  
QY 61 VPGKEVNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVLGLGVGTG 120  
DB 61 VPGKEVNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVLGLGVGTG 120  
QY 121 NGTRLVVEKEHPOLG 135  
DB 121 NGTRLVVEKEHPOLG 135

RESULT 11  
US-10-036-444-4  
; Sequence 4, Application US/10036444  
; Publication No. US20020142445A1  
; GENERAL INFORMATION:  
; APPLICANT: INNATE PHARMA S.A.S.  
; APPLICANT: UNIVERSITA DI GENOVA  
; TITLE OF INVENTION: "No. US20020142445A1el triggering receptor involved in natural  
; TITLE OF INVENTION: cytotoxicity mediated by human Natural Killer cells and  
; TITLE OF INVENTION: antibodies that identify the same"  
; FILE REFERENCE: SEQ-PR-1060  
; CURRENT APPLICATION NUMBER: US/10/036,444  
; CURRENT FILING DATE: 2002-01-07  
; PRIOR APPLICATION NUMBER: 09/440,514  
; PRIOR FILING DATE: 1999-11-15  
; PRIOR APPLICATION NUMBER: 09/456,199  
; PRIOR FILING DATE: 1999-12-07  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 120  
; TYPE: PRT  
; ORGANISM: Human NK cell  
US-10-036-444-4

Query Match 62.0%; Score 632; DB 13; Length 120;  
Best Local Similarity 100.0%; Pred. No. 7.3e-55;  
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 59 EWVPEKVR-----NGTPEFRGLAP-----LASSRFLHDHQAELHVRGHDAS 104  
DB 58 R--FGKGRFVVRVGTGCVWVGRGADIPDRFVSVSGSLNRF-----LIRNIEEDES 108  
QY 105 IYVCEVEVLGIGVGT-----GNGTRLVW-----EKEHPOLGAGTIVLL 142  
DB 109 DYHCGTD---LGSCTSFVSVWVFGGTKLTVLSQPKAAPSVTLPFPSSSELOANKATLVCL 165  
QY 143 RAGFY 147  
DB 166 ISDFY 170

RESULT 14  
US-10-225-108A-12  
; Sequence 12, Application US/10225108A  
; Publication No. US20030157112A1  
; GENERAL INFORMATION:  
; APPLICANT: HOOPER, Craig  
; APPLICANT: DIETZSCHOLD, Bernhard  
; TITLE OF INVENTION: Recombinant Antibodies, and Compositions  
; TITLE OF INVENTION: and Methods for Making Them  
; FILE REFERENCE: 8321-110  
; CURRENT APPLICATION NUMBER: US/10/225.108A  
; CURRENT FILING DATE: 2003-04-10  
; PRIOR APPLICATION NUMBER: US 09/848,832  
; PRIOR FILING DATE: 2001-05-04  
; PRIOR APPLICATION NUMBER: US 60/204,518  
; PRIOR FILING DATE: 2001-05-16  
; PRIOR APPLICATION NUMBER: US 60/314,023  
; PRIOR FILING DATE: 2001-08-21  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12  
; LENGTH: 232  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-225-108A-12

Query Match 11.7%; Score 119.5; DB 14; Length 232;  
Best Local Similarity 26.0%; Pred. No. 0.0017;  
Matches 45; Conservative 25; Mismatches 64; Indels 39; Gaps 7;

QY 1 MAWMLLLILIMVH-PCSCALWV-SQPEIRTLGSSAFPCSFNASQGRLAIGSVTWFRD 58  
DB 1 MAWTVLLGLLSHCTGTSVTVLTQPPSVVAPGKTARINCNGNNIEYR---SVHWYQQ 56  
QY 59 E-----VPEKVRNGTPE-FRGLAPLASSRFLHDHQAELHVRGHDASIVYCR 109  
DB 57 KSGQAPVAVIYDNRPSGIPERFSGSKS-----GNTATLTISRVEAGDEADYVQC 107  
QY 110 VEVLGIGVGTGNGTRLVW-----EKEHPOLGAGTIVLLRAGFY 147  
DB 108 VWDISSDVVFGGTKLTVLSQPKAAPSVTLPFPSSSELOANKATLVCLISDFY 160

RESULT 15  
US-10-461-148-6  
; Sequence 6, Application US/10461148  
; Publication No. US20040013672A1  
; GENERAL INFORMATION:  
; APPLICANT: Dietzschold, Bernhard  
; APPLICANT: Hooper, Douglas C.  
; TITLE OF INVENTION: RECOMBINANT ANTIBODIES AND COMPOSITIONS  
; TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THE SAME  
; FILE REFERENCE: 8321-110C11-185685  
; CURRENT APPLICATION NUMBER: US/10/461,148  
; CURRENT FILING DATE: 2003-06-13  
; PRIOR APPLICATION NUMBER: US 10/225.108  
; PRIOR FILING DATE: 2002-08-21  
; PRIOR APPLICATION NUMBER: US 60/314,023  
; PRIOR FILING DATE: 2001-08-21

QY 19 LWVSQPEIRTLGSSAFPCSFNASQGRLAIGSVTWFRDDEVVPGKEVRNGTPEFRGLA 78  
DB 1 LWVSQPEIRTLGSSAFPCSFNASQGRLAIGSVTWFRDDEVVPGKEVRNGTPEFRGLA 60  
QY 79 PLASSRFLHDHQAELHVRGHDASIVYCRVEVLGIGVGTGNGTRLVVEKEHPOLGAGT 138  
DB 61 PLASSRFLHDHQAELHVRGHDASIVYCRVEVLGIGVGTGNGTRLVVEKEHPOLGAGT 120

RESULT 12  
US-10-036-444-6  
; Sequence 6, Application US/10036444  
; Publication No. US20020142445A1  
; GENERAL INFORMATION:  
; APPLICANT: INNATE PHARMA S.A.S.  
; APPLICANT: UNIVERSITA DI GENOVA  
; TITLE OF INVENTION: "No. US20020142445A1el triggering receptor involved in natural  
; TITLE OF INVENTION: cytotoxicity mediated by human Natural Killer cells and  
; TITLE OF INVENTION: antibodies that identify the same"  
; FILE REFERENCE: SEQ-PR-1060  
; CURRENT APPLICATION NUMBER: US/10/036,444  
; CURRENT FILING DATE: 2002-01-07  
; PRIOR APPLICATION NUMBER: 09/440,514  
; PRIOR FILING DATE: 1999-11-15  
; PRIOR APPLICATION NUMBER: 09/456,199  
; PRIOR FILING DATE: 1999-12-07  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 33  
; TYPE: PRT  
; ORGANISM: Human NK cell  
US-10-036-444-6

Query Match 20.0%; Score 204; DB 13; Length 33;  
Best Local Similarity 100.0%; Pred. No. 5.8e-13;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 158 STVYQKCHCHMGTHCHSSDGRGVPEPRCP 190  
DB 1 STVYQKCHCHMGTHCHSSDGRGVPEPRCP 33

RESULT 13  
US-09-909-567B-49  
; Sequence 49, Application US/09909567B  
; Publication No. US20030022257A1  
; GENERAL INFORMATION:  
; APPLICANT: Macina, Roberto A.  
; APPLICANT: Nair, Manoj  
; APPLICANT: Cher, Seiyu  
; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes  
; FILE REFERENCE: DEX-0214  
; CURRENT APPLICATION NUMBER: US/09/909,567B  
; CURRENT FILING DATE: 2001-07-20  
; PRIOR APPLICATION NUMBER: 60/219,834  
; PRIOR FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 49  
; LENGTH: 246  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-909-567B-49

Query Match 12.1%; Score 123.5; DB 10; Length 246;  
Best Local Similarity 29.2%; Pred. No. 0.00073;  
Matches 54; Conservative 17; Mismatches 61; Indels 53; Gaps 10;

QY 1 MAWMLLLILIMVH-PCSCALWV-SQPEIRTLGSSAFPCSFNASQGRLAIGSVTWFRD 58  
DB 1 MAWAPLLTLTLLTGLSLSQPILTOPPSASASLGASVTLCVSVDYKVL---EVDNFQ 57



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OM protein - protein search, using sw model  
Run on: November 16, 2004, 19:04:36 ; Search time 53.4218 Seconds  
(without alignments)  
235.867 Million cell updates/sec

Title: US-10-036-444-2  
Perfect score: 1020  
Sequence: 1 MAWMLLLILIMVHPCALW.....GTHCHSDGPRGVPEPRCP 190

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66319000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:  
1: /cgn2\_6/protdata/1/iaa/5A COMB.pcp.\*  
2: /cgn2\_6/protdata/1/iaa/5B COMB.pcp.\*  
3: /cgn2\_6/protdata/1/iaa/6A COMB.pcp.\*  
4: /cgn2\_6/protdata/1/iaa/6B COMB.pcp.\*  
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6: /cgn2\_6/protdata/1/iaa/backfiles1.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	112	11.0	223	3	US-08-228-208A-17
2	111.5	10.9	226	4	US-09-311-784A-32
3	106.5	10.4	364	4	US-09-472-087-100
4	106	10.4	270	3	US-09-082-593-10
5	104.5	10.2	238	4	US-09-227-595-30
6	104.5	10.2	238	4	US-09-227-595-32
7	104.5	10.2	238	4	US-08-595-590B-30
8	104.5	10.2	238	4	US-08-595-590B-32
9	104	10.2	174	3	US-08-804-180C-4
10	103.5	10.1	187	1	US-08-067-684-14
11	103.5	10.1	187	1	US-08-068-898-14
12	103.5	10.1	187	2	US-08-459-818-14
13	103.5	10.1	187	2	US-08-889-666-14
14	103.5	10.1	187	2	US-08-465-078-14
15	103.5	10.1	187	2	US-08-725-776-14
16	103.5	10.1	187	2	US-08-488-062-14
17	103.5	10.1	187	3	US-08-228-208A-14
18	103.5	10.1	187	4	US-08-223-783-36
19	103.5	10.1	187	5	PCT-US95-06726-36
20	103.5	10.1	236	3	US-09-049-672A-7
21	103	10.1	267	1	US-08-416-336-2
22	102.5	10.0	223	4	US-09-303-040-10
23	101.5	10.0	374	4	US-09-227-595-26
24	101.5	10.0	374	4	US-08-227-595-28
25	101.5	10.0	374	4	US-08-595-590B-26
26	101.5	10.0	374	4	US-08-595-590B-28
27	101.5	10.0	377	4	US-09-227-595-24

28	101.5	10.0	377	4	US-08-595-590B-24
29	100	9.8	239	4	US-09-828-995B-26
30	98.5	9.7	526	4	US-09-910-174B-9
31	98.5	9.7	526	4	US-09-820-461-9
32	98	9.6	589	2	US-08-724-394A-1
33	97	9.5	131	1	US-08-305-683A-4
34	97	9.5	253	2	US-08-459-818-20
35	97	9.5	253	2	US-08-889-666-20
36	97	9.5	253	2	US-08-465-078-20
37	97	9.5	253	2	US-08-725-776-20
38	97	9.5	253	2	US-08-488-062-20
39	97	9.5	502	2	US-08-459-818-19
40	97	9.5	502	2	US-08-889-666-19
41	97	9.5	502	2	US-08-465-078-19
42	97	9.5	502	2	US-08-725-776-19
43	97	9.5	502	2	US-08-488-062-19
44	95.5	9.4	218	4	US-10-026-045-1
45	95.5	9.4	218	4	US-10-026-045-2

ALIGNMENTS

RESULT 1  
US-08-228-208A-17  
; Sequence 17, Application US/06228208A  
; Patent No. 6090914  
; GENERAL INFORMATION:  
; APPLICANT: Linsley, Peter S.  
; APPLICANT: Ledbetter, Jeffrey A.  
; APPLICANT: Dams, Nitin K.  
; APPLICANT: Brady, William  
; APPLICANT: Wallace, Philip M.  
; TITLE OF INVENTION: CTLA4/CD28ig HYBRID FUSION  
; TITLE OF INVENTION: PROTEINS AND USES THEREOF  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant & Gould  
; STREET: 1150 Santa Monica Boulevard, Suite 400  
; CITY: Los Angeles  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 90025  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/228,208A  
; FILING DATE: 15-APR-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/008,898  
; FILING DATE: 22-JAN-1993  
; APPLICATION NUMBER: 07/723,617  
; FILING DATE: 27-JUN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Adriano, Sarah B  
; REGISTRATION NUMBER: 34,470  
; REFERENCE/DOCKET NUMBER: 30436-30US01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 310 445-1140  
; TELEFAX: 310 445-9031  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 223 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-228-208A-17

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Sequence 26, Appl  
Sequence 9, Appl  
Sequence 9, Appl  
Sequence 1, Appl  
Sequence 4, Appl  
Sequence 20, Appl  
Sequence 20, Appl  
Sequence 20, Appl  
Sequence 20, Appl  
Sequence 19, Appl  
Sequence 19, Appl  
Sequence 1, Appl  
Sequence 2, Appl

Query Match 11.0%; Score 112; DB 3; Length 223;  
Best Local Similarity 28.0%; Pred. No. 0.00059;  
Matches 47; Conservative 22; Mismatches 75; Indels 24; Gaps 6;  
  
QY 6 LLLILIMVHGSC-ALMYSQPEIRTLGSSAFPLPCSFNASQGLAIGSVTFWFRDEVVPGK 64  
DB 24 LFFELLIPVCKAMHVAQPAVLAASSRGIAASFVCEY-ASPGKATEVRVTVLQADSQVT 82  
QY 65 EVRNGTPEFRGRGLAPLASSRFLHD-----HQAEHLHIRDVGHDAIYVCRVRL-- 113  
DB 83 EVCAATYMGNELT-----FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMYP 136  
QY 114 -GLGVGTGNGTRLVVEKEHQPGLGAGTVLLARA-----CFYAVSFLSVAV 156  
DB 137 PPYILGIGNGTQIYVIDPECPDSDFLMLLAIVSSGLFFYSFLLTAV 184  
  
RESULT 2  
US-09-311-784A-32  
; Sequence 32, Application US/09311784A  
; Patent No. 6534462  
; GENERAL INFORMATION:  
; APPLICANT: Fikes, John D.  
; APPLICANT: Hermanson, Gary G.  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Ishioka, Glenn Y.  
; APPLICANT: Livingston, Brian  
; APPLICANT: Chesnut, Robert W.  
; APPLICANT: Epimmune Inc.  
; TITLE OF INVENTION: Expression Vectors for Stimulating an  
; TITLE OF INVENTION: Immune Response and Methods of Using the Same  
; FILE REFERENCE: 39963-20022.01  
; CURRENT APPLICATION NUMBER: US/09/311,784A  
; CURRENT FILING DATE: 1999-05-13  
; PRIOR FILING DATE: 1999-05-13  
; NUMBER OF SEQ ID NOS: 463  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 32  
; LENGTH: 226  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: human MB-1 Ig-alpha  
US-09-311-784A-32

Query Match 10.9%; Score 111.5; DB 4; Length 226;  
Best Local Similarity 28.0%; Pred. No. 0.00067;  
Matches 47; Conservative 24; Mismatches 70; Indels 27; Gaps 8;  
  
QY 4 MLLILIMVHGSCALWVQ-PEIRTLGSSAFPLPCSFNASQGLAIGSVTFWFRDEVV 62  
DB 18 LFLLSAVYLGPGCQALMHWKVPASLVSLGDAHFQCPHNSNN---ANVTWWR--VLH 71  
QY 63 GKEVRNGT--PEFRGRGLAPLASSRFLHDQAEHLHIRDVGHDAIYVCRVRLGLGVGTG 120  
DB 72 G-----NYTWPPPELGP-----CEDPNGTLLIQNVNKGHGIYVCRVQEGNESYQOS 118  
QY 121 NGTRLVVEKEHPQ-----LGAGTV-LLLRAGFYAVSFLSVAVGSTVYVQ 163  
DB 119 CGTYLAVRQPPPPFPFDMGEGTKNRIITAEGIILLFCAVVPGLTLFR 166

RESULT 3  
US-09-472-087-100  
; Sequence 100, Application US/09472087  
; Patent No. 6682736  
; GENERAL INFORMATION:  
; APPLICANT: HANSON, DOUGLAS C.  
; APPLICANT: NEVEU, MARK J.  
; APPLICANT: MUELLER, EILEEN E.  
; APPLICANT: HANKE, JEFFREY H.

; APPLICANT: GILMAN, STEVEN C.  
; APPLICANT: DAVIS, C. GEOFFREY  
; APPLICANT: CORVALAN, JOSE R.  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4  
; FILE REFERENCE: ABX-PFI  
; CURRENT APPLICATION NUMBER: US/09/472,087  
; CURRENT FILING DATE: 1999-12-23  
; PRIOR FILING DATE: 60/113,647  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 100  
; LENGTH: 364  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; ORGANISM: Homo sapiens  
US-09-472-087-100

Query Match 10.4%; Score 106.5; DB 4; Length 364;  
Best Local Similarity 28.0%; Pred. No. 0.0044;  
Matches 40; Conservative 20; Mismatches 62; Indels 21; Gaps 5;  
  
QY 4 MLLILIMVHP--GSCALWVSQPEIRTLGSSAFPLPCSFNASQGLAIGSVTFWFRDEVV 61  
DB 10 LLSLVALLFPMSMASMAHVAQPAVLAASSRGIAASFVCEY-ASPGKATEVRVTVLQADS 68  
QY 62 PGKEVRNGTPEFRGRGLAPLASSRFLHD-----HQAEHLHIRDVGHDAIYVCRVRE 112  
DB 69 QVTEVCAATYMGNELT-----FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVEL 122  
QY 113 L---GLGVGTGNGTRLVVEKEHP 132  
DB 123 MYPPPYLIGNGTQIYVIDPEP 145

RESULT 4  
US-09-082-593-10  
; Sequence 10, Application US/09082593  
; Patent No. 6180104  
; GENERAL INFORMATION:  
; APPLICANT: DAVIS, MARK M.  
; APPLICANT: HEDRICK, STEPHEN M.  
; TITLE OF INVENTION: T CELL RECEPTOR BETA SUBUNIT  
; FILE REFERENCE: JX1193-195DIV2  
; CURRENT APPLICATION NUMBER: US/09/082,593  
; CURRENT FILING DATE: 1998-05-20  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 270  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-082-593-10

Query Match 10.4%; Score 106; DB 3; Length 270;  
Best Local Similarity 25.8%; Pred. No. 0.0033;  
Matches 40; Conservative 22; Mismatches 45; Indels 48; Gaps 9;  
  
QY 3 WMLLILIMVHGSCALWVS-----QPPEIRTLGSSAFPLPCSFNASQGLAIGSVTW 55  
DB 12 WLLL-----NWVNSQNVQSPESLIVPEGARTSLNCTPSDSASQY-----FWW 55  
QY 56 FREVVPKGKVR-----NGTEFRGRGLAPLASSRFLHDQAEHLHIRDVGHDAIYVCR 108  
DB 56 YRQH--SGKAPKALMIFNSGEKE-BGRFTTHINKASLH---FSLHIRDSQPSDSALYLC 109  
QY 109 RVEVLGLGVGTGNGTRLVVEKEHPQLGAGTVLLLR 143  
DB 110 AVTLYG-----GSGNKLI-----FGTGLLSVK 132

RESULT 5  
US-09-227-595-30  
; Sequence 30, Application US/09227595

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; Patent No. 6444792
; GENERAL INFORMATION:
; APPLICANT: Gray, Gary S. et al.
; TITLE OF INVENTION: CTLA4-Immunoglobulin Fusion Proteins
; TITLE OF INVENTION: Having Modified Effector Functions and Uses Therefor
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/227,595
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/595,590
; FILING DATE: February 2, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 238 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-09-227-595-30

Query Match 10.2%; Score 104.5; DB 4; Length 238;
Best Local Similarity 24.7%; Pred. No. 0.0041;
Matches 43; Conservative 24; Mismatches 70; Indels 37; Gaps 7;

QY 1 MAWMLLLILIM-----VHPGSCALWVSQPPEIRTLGSSAFPLPCSFNASQGRLAIGSVTW 55
Db 1 MGWSCIILFLVATATGVH---SAMHVAQPAVVLASSRGIASFVCEY-ASPGKATEVRVTV 56
QY 56 FRDEVVPGKEVRNGTPEFRGRLAFLASSRFLHD-----HQAELHIRDVRGHDASIY 106
Db 57 LRQADSQVTEVCAATYMMGNELT-----FLDDSICTGTSSGNQVNLTIQGLRAMDTGLY 110
QY 107 VCRVEVL---GLGVGTGNGTRLV-----EKEHPQLGAGTVLLLRAGFY 147
Db 111 ICKVELMYPYPYILGIGNGAQITVAAPSVFIFFPPSDEQLKSGTASVCLLNIFY 164

RESULT 6
US-09-227-595-32
; Sequence 32, Application US/09227595
; Patent No. 6444792
; GENERAL INFORMATION:
; APPLICANT: Gray, Gary S. et al.
; TITLE OF INVENTION: CTLA4-Immunoglobulin Fusion Proteins
; TITLE OF INVENTION: Having Modified Effector Functions and Uses Therefor
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA

; Patent No. 6444792
; GENERAL INFORMATION:
; APPLICANT: Gray, Gary S. et al.
; TITLE OF INVENTION: CTLA4-Immunoglobulin Fusion Proteins
; TITLE OF INVENTION: Having Modified Effector Functions and Uses Therefor
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-Windows
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,590B
; FILING DATE: 02-Feb-1996
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
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; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/227,595
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/595,590
; FILING DATE: February 2, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 238 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-09-227-595-32

Query Match 10.2%; Score 104.5; DB 4; Length 238;
Best Local Similarity 24.7%; Pred. No. 0.0041;
Matches 43; Conservative 24; Mismatches 70; Indels 37; Gaps 7;

QY 1 MAWMLLLILIM-----VHPGSCALWVSQPPEIRTLGSSAFPLPCSFNASQGRLAIGSVTW 55
Db 1 MGWSCIILFLVATATGVH---SAMHVAQPAVVLASSRGIASFVCEY-ASPGKATEVRVTV 56
QY 56 FRDEVVPGKEVRNGTPEFRGRLAFLASSRFLHD-----HQAELHIRDVRGHDASIY 106
Db 57 LRQADSQVTEVCAATYMMGNELT-----FLDDSICTGTSSGNQVNLTIQGLRAMDTGLY 110
QY 107 VCRVEVL---GLGVGTGNGTRLV-----EKEHPQLGAGTVLLLRAGFY 147
Db 111 ICKVELMYPYPYILGIGNGAQITVAAPSVFIFFPPSDEQLKSGTASVCLLNIFY 164

RESULT 7
US-08-595-590B-30
; Sequence 30, Application US/08595590B
; Patent No. 6750334
; GENERAL INFORMATION:
; APPLICANT: Gray, Gary S. et al.
; TITLE OF INVENTION: CTLA4-Immunoglobulin Fusion Proteins
; Having Modified Effector Functions and Uses Therefor
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-Windows
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,590B
; FILING DATE: 02-Feb-1996
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-007CPA2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 238 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-08-595-590B-30

Query Match 10.2%; Score 104.5; DB 4; Length 238;
Best Local Similarity 24.7%; Pred. No. 0.0041;
Matches 43; Conservative 24; Mismatches 70; Indels 37; Gaps 7;

QY 1 MAWMLLLILIM-----VHPSGSCALWVSOPPEIRLTGSSAFPLCSFNASQRLAIGSVTW 55
Db 1 MGWSCIILFLVATATGVH---SAMHVAQPAVAVLASSRGIAFVCEY-ASPGKATEVRVTV 56
QY 56 FRDEVPGKEVRNGTPEFRGLAPLASSRFLHD-----HQAELHIRDVRGHDASIY 106
Db 57 LRQADSQVTEVCAATYMGNELT-----FLDSDICTGTSSGNQVNLTIQGLRAMDTGLY 110
QY 107 VCRVEVL---GLGVGTGNGTRLV-----EKEHPQLGAGTVLLLRAGFY 147
Db 111 ICKVELMYPYPYILGIGNGAQITVAAPSVFIFFPPSDQLKSGTASVVCLNNFY 164

RESULT 8
US-08-595-590B-32
; Sequence 32, Application US/08595590B
; Patent No. 6750334
; GENERAL INFORMATION:
; APPLICANT: Gray, Gary S. et al.
; TITLE OF INVENTION: CTLA4-Immunoglobulin Fusion Proteins
; Having Modified Effector Functions and Uses
; Therefor
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-Windows
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,590B
; FILING DATE: 02-Feb-1996
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-007CPA2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 32:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-007CPA2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 238 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-08-595-590B-32

Query Match 10.2%; Score 104.5; DB 4; Length 238;
Best Local Similarity 24.7%; Pred. No. 0.0041;
Matches 43; Conservative 24; Mismatches 70; Indels 37; Gaps 7;

QY 1 MAWMLLLILIM-----VHPSGSCALWVSOPPEIRLTGSSAFPLCSFNASQRLAIGSVTW 55
Db 1 MGWSCIILFLVATATGVH---SAMHVAQPAVAVLASSRGIAFVCEY-ASPGKATEVRVTV 56
QY 56 FRDEVPGKEVRNGTPEFRGLAPLASSRFLHD-----HQAELHIRDVRGHDASIY 106
Db 57 LRQADSQVTEVCAATYMGNELT-----FLDSDICTGTSSGNQVNLTIQGLRAMDTGLY 110
QY 107 VCRVEVL---GLGVGTGNGTRLV-----EKEHPQLGAGTVLLLRAGFY 147
Db 111 ICKVELMYPYPYILGIGNGAQITVAAPSVFIFFPPSDQLKSGTASVVCLNNFY 164

RESULT 9
US-08-804-180C-4
; Sequence 4, Application US/08804180C
; Patent No. 6107056
; GENERAL INFORMATION:
; APPLICANT: Martin K. Oaks
; TITLE OF INVENTION: sCTLA-4 and Its Soluble Products
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Thomas M. Wozny
; STREET: 100 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.50 inch Disk
; COMPUTER: IBM
; OPERATING SYSTEM: DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/804,180C
; FILING DATE: February 20, 1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas M. Wozny
; REGISTRATION NUMBER: 28,922
; REFERENCE/DOCKET NUMBER: 3284-00003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 271-7590
; TELEFAX: (414) 271-5770
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 174
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Polypeptide
; DESCRIPTION: no
; HYPOTHETICAL: no
; FRAGMENT TYPE: Internal fragment
; ORIGINAL SOURCE:
; ORGANISM: Rattus No. 6107056vegicus
; STRAIN: ACI
; DEVELOPMENTAL STAGE: Adult
; CELL TYPE: Splenocyte
; FEATURE:
; NAME/KEY: Rat sCTLA-4
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```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 238 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-08-595-590B-32

Query Match 10.2%; Score 104.5; DB 4; Length 238;
Best Local Similarity 24.7%; Pred. No. 0.0041;
Matches 43; Conservative 24; Mismatches 70; Indels 37; Gaps 7;

QY 1 MAWMLLLILIM-----VHPSGSCALWVSOPPEIRLTGSSAFPLCSFNASQRLAIGSVTW 55
Db 1 MGWSCIILFLVATATGVH---SAMHVAQPAVAVLASSRGIAFVCEY-ASPGKATEVRVTV 56
QY 56 FRDEVPGKEVRNGTPEFRGLAPLASSRFLHD-----HQAELHIRDVRGHDASIY 106
Db 57 LRQADSQVTEVCAATYMGNELT-----FLDSDICTGTSSGNQVNLTIQGLRAMDTGLY 110
QY 107 VCRVEVL---GLGVGTGNGTRLV-----EKEHPQLGAGTVLLLRAGFY 147
Db 111 ICKVELMYPYPYILGIGNGAQITVAAPSVFIFFPPSDQLKSGTASVVCLNNFY 164

RESULT 9
US-08-804-180C-4
; Sequence 4, Application US/08804180C
; Patent No. 6107056
; GENERAL INFORMATION:
; APPLICANT: Martin K. Oaks
; TITLE OF INVENTION: sCTLA-4 and Its Soluble Products
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Thomas M. Wozny
; STREET: 100 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.50 inch Disk
; COMPUTER: IBM
; OPERATING SYSTEM: DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/804,180C
; FILING DATE: February 20, 1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas M. Wozny
; REGISTRATION NUMBER: 28,922
; REFERENCE/DOCKET NUMBER: 3284-00003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 271-7590
; TELEFAX: (414) 271-5770
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 174
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Polypeptide
; DESCRIPTION: no
; HYPOTHETICAL: no
; FRAGMENT TYPE: Internal fragment
; ORIGINAL SOURCE:
; ORGANISM: Rattus No. 6107056vegicus
; STRAIN: ACI
; DEVELOPMENTAL STAGE: Adult
; CELL TYPE: Splenocyte
; FEATURE:
; NAME/KEY: Rat sCTLA-4
```

IDENTIFICATION METHOD: Found by experiment  
OTHER INFORMATION: B7 binding protein  
US-08-804-180C-4

Query Match 10.2%; Score 104; DB 3; Length 174;  
Best Local Similarity 29.7%; Pred. No. 0.003;  
Matches 41; Conservative 23; Mismatches 56; Indels 18; Gaps 7;  
QY 5 LLILLINWFGSCALWVSOPPEIRTELGSSAFPC---SFNASQGRLAIGSVTWFRDEV 60  
DB 24 VLUSLUFIPFSAIQOTQSVVLASHGVASFCEYASHNTDEVRTVLKQT--NDQV 81  
QY 61 VPKVEKNGTPPEFRGLA----PLASSRFLHQAELHIRDVRGHDASIYVCRVEVL--- 113  
DB 82 T---EVCATFTVKNTLGFLLDDPFCGTF-NESRVNLTIGLRADTGLYFCKVELMYPP 137  
QY 114 GLGVGTGNGTRL-VVEKE 130  
DB 138 PYFVGMGNGTQIYIAKE 155

RESULT 10  
US-08-067-684-14  
; Sequence 14, Application US/08067684  
; Patent No. 5434131  
; GENERAL INFORMATION:  
; APPLICANT: Linsley, Peter S.  
; APPLICANT: Ledbetter, Jeffrey A.  
; APPLICANT: Damle, Nitin K.  
; APPLICANT: Brady, William  
; TITLE OF INVENTION: CTLA4 RECEPTOR AND METHODS FOR ITS USE  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sheldon & Mak  
; STREET: 225 South Lake Avenue, Suite 900  
; CITY: Pasadena  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 91101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/067,684  
; FILING DATE: 26-MAY-1993  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Adriano, Sarah B.  
; REGISTRATION NUMBER: 34,470  
; REFERENCE/DOCKET NUMBER: 7848-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 310/312-9900  
; TELEFAX: 310/479-8340  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 187 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-08-067-684-14

Query Match 10.1%; Score 103.5; DB 1; Length 187;  
Best Local Similarity 27.7%; Pred. No. 0.0038;  
Matches 43; Conservative 20; Mismatches 69; Indels 23; Gaps 5;  
QY 18 ALWVSQPEIRTELGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPFRGRL 77  
DB 1 AMHVAQPAVVLASSRGIASFVCEY-ASPGKATEVTVTLROADSQVTEVCAATYMGNEL 59

QY 78 APLASSRFLHD-----HQAELHIRDVRGHDASIYVCRVEVL---GLGVGTGNGTRL 125  
DB 60 T-----FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMYPPIYVIGNGTQI 113  
QY 126 VVEKEHPQAGTAVLLRA-----GFYAVSFSLVAV 156  
DB 114 YVIDPEPCDSDFLMLILAAVSSGLFFYSFLLTAV 148

RESULT 11  
US-08-008-898-14  
; Sequence 14, Application US/08008898  
; Patent No. 5770197  
; GENERAL INFORMATION:  
; APPLICANT: Linsley, Peter S.  
; APPLICANT: Ledbetter, Jeffrey A.  
; APPLICANT: Damle, Nitin K.  
; APPLICANT: Brady, William  
; TITLE OF INVENTION: CTLA4 RECEPTOR AND METHODS FOR ITS USE  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sheldon & Mak  
; STREET: 201 South Lake Avenue, Suite 800  
; CITY: Pasadena  
; STATE: California  
; COUNTRY: United States  
; ZIP: 91101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/008,898  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/723,617  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mandel, SaraLynn  
; REGISTRATION NUMBER: 31,853  
; REFERENCE/DOCKET NUMBER: 7848  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (818) 796-4000  
; TELEFAX: (818) 795-6321  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 187 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-008-898-14

Query Match 10.1%; Score 103.5; DB 1; Length 187;  
Best Local Similarity 27.7%; Pred. No. 0.0038;  
Matches 43; Conservative 20; Mismatches 69; Indels 23; Gaps 5;  
QY 18 ALWVSQPEIRTELGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPFRGRL 77  
DB 1 AMHVAQPAVVLASSRGIASFVCEY-ASPGKATEVTVTLROADSQVTEVCAATYMGNEL 59  
QY 78 APLASSRFLHD-----HQAELHIRDVRGHDASIYVCRVEVL---GLGVGTGNGTRL 125  
DB 60 T-----FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMYPPIYVIGNGTQI 113

RESULT 12  
US-08-459-818-14

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; Sequence 14, Application US/08459818
; Patent No. 5851795
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Damle, Nitin K.
; APPLICANT: Brady, William
; TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Blvd., Suite 400
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FastSeq 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,818
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; NAME: Adriano, Sarah B.
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436.35US02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 187 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-459-818-14

Query Match          10.1%; Score 103.5; DB 2; Length 187;
Best Local Similarity 27.7%; Pred. No. 0.0038;
Matches 43; Conservative 20; Mismatches 69; Indels 23; Gaps 5;

QY 18 ALWVSQPEIRTELGSSAFPCSNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGL 77
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 1 AMHVAQPAVVLASSRGIASFVCEY-ASPGKATEVRVTVLRLQADSQVTEVCAATYMMGNEL 59

QY 78 APLASSRFLHD-----HQAELHIRDVRGHDASIVYCRVEVL---GLGVGTGNGTRL 125
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 60 T-----FLDSDICTGSSGNQNLITQGRAMDTGLYICKVELMYPYPYLGINGTQI 113

QY 126 VVEKEHPOLGAGTVLLRA----GFYAVSFLSVAV 156
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 114 YVIDPEPCDSDFLWLILAAVSSGLPFYSFLLTAV 148

RESULT 13
US-08-889-666-14
; Sequence 14, Application US/08889666
; Patent No. 5885579
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Damle, Nitin K.
; APPLICANT: Brady, William
; APPLICANT: Kiener, Peter A.
; TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Blvd., Suite 400
; CITY: Los Angeles
```

```
; STATE: California
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/889,666
; FILING DATE: 08-JUL-1997
; CLASSIFICATION: 435
; NAME: Adriano, Sarah B.
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436-35US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 187 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-889-666-14

Query Match          10.1%; Score 103.5; DB 2; Length 187;
Best Local Similarity 27.7%; Pred. No. 0.0038;
Matches 43; Conservative 20; Mismatches 69; Indels 23; Gaps 5;

QY 18 ALWVSQPEIRTELGSSAFPCSNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGL 77
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 1 AMHVAQPAVVLASSRGIASFVCEY-ASPGKATEVRVTVLRLQADSQVTEVCAATYMMGNEL 59

QY 78 APLASSRFLHD-----HQAELHIRDVRGHDASIVYCRVEVL---GLGVGTGNGTRL 125
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 60 T-----FLDSDICTGSSGNQNLITQGRAMDTGLYICKVELMYPYPYLGINGTQI 113

QY 126 VVEKEHPOLGAGTVLLRA----GFYAVSFLSVAV 156
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 114 YVIDPEPCDSDFLWLILAAVSSGLPFYSFLLTAV 148

RESULT 14
US-08-465-078-14
; Sequence 14, Application US/08465078
; Patent No. 5885796
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Damle, Nitin K.
; APPLICANT: Brady, William
; APPLICANT: Kiener, Peter A.
; TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Blvd., Suite 400
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/465,078
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/375390
; FILING DATE: 18-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B.
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436-35US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 187 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-465-078-14

Query Match          10.1%; Score 103.5; DB 2; Length 187;
Best Local Similarity 27.7%; Pred. No. 0.0038;
Matches 43; Conservative 20; Mismatches 69; Indels 23; Gaps 5;

QY 18 ALWVSQPEIRTLGSSAFPCSNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGRL 77
Db 1 AMHVAQPAVVLASSRGIASFVCEY-ASPGKATEVRVTVLRLQADSQVTEVCAATYMGNEL 59
QY 78 APLASSRFLHD-----HQAEHLHTRVGRHDASIYVCRVEVL---GLGVGTGNGTRL 125
Db 60 T-----FLDDBSICGTSSGNQVNLTIQGLRAMDTGLYICKVELMYPYPYVLGIGNGTQI 113
QY 126 VVEKEHPQLGAGTVLLRA---GFYAVSFLSVAV 156
Db 114 YVIDPEPCDSDFLWLILAAVSSGLFFYSFLTAV 148

; APPLICATION NUMBER: US/08/465,078
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/375390
; FILING DATE: 18-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B.
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436-35US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 187 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-465-078-14

Query Match          10.1%; Score 103.5; DB 2; Length 187;
Best Local Similarity 27.7%; Pred. No. 0.0038;
Matches 43; Conservative 20; Mismatches 69; Indels 23; Gaps 5;

QY 18 ALWVSQPEIRTLGSSAFPCSNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGRL 77
Db 1 AMHVAQPAVVLASSRGIASFVCEY-ASPGKATEVRVTVLRLQADSQVTEVCAATYMGNEL 59
QY 78 APLASSRFLHD-----HQAEHLHTRVGRHDASIYVCRVEVL---GLGVGTGNGTRL 125
Db 60 T-----FLDDBSICGTSSGNQVNLTIQGLRAMDTGLYICKVELMYPYPYVLGIGNGTQI 113
QY 126 VVEKEHPQLGAGTVLLRA---GFYAVSFLSVAV 156
Db 114 YVIDPEPCDSDFLWLILAAVSSGLFFYSFLTAV 148

; APPLICATION NUMBER: US/08/465,078
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/375390
; FILING DATE: 18-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B.
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436-35US01
```

```
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 187 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-725-776-14

Query Match          10.1%; Score 103.5; DB 2; Length 187;
Best Local Similarity 27.7%; Pred. No. 0.0038;
Matches 43; Conservative 20; Mismatches 69; Indels 23; Gaps 5;

QY 18 ALWVSQPEIRTLGSSAFPCSNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGRL 77
Db 1 AMHVAQPAVVLASSRGIASFVCEY-ASPGKATEVRVTVLRLQADSQVTEVCAATYMGNEL 59
QY 78 APLASSRFLHD-----HQAEHLHTRVGRHDASIYVCRVEVL---GLGVGTGNGTRL 125
Db 60 T-----FLDDBSICGTSSGNQVNLTIQGLRAMDTGLYICKVELMYPYPYVLGIGNGTQI 113
QY 126 VVEKEHPQLGAGTVLLRA---GFYAVSFLSVAV 156
Db 114 YVIDPEPCDSDFLWLILAAVSSGLFFYSFLTAV 148

Search completed: November 16, 2004, 19:17:42
Job time : 54.4215 secs
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RESULT 15
US-08-725-776-14
; Sequence 14, Application US/08725776
; Patent No. 5968510
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Damle, Nitin K.
; APPLICANT: Brady, William
; APPLICANT: Kiener, Peter A.
; TITLE OF INVENTION: C11A4 Receptor and Uses Thereof
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Blvd., Suite 400
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/725,776
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/375390
; FILING DATE: 18-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B.
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436-35US01
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model  
Run on: November 16, 2004, 18:56:40 ; Search time 24.8276 Seconds  
(without alignments)  
465.048 Million cell updates/sec  
Title: US-10-036-444-4  
Perfect score: 632  
Sequence: 1 LWSQPPEIRTELGSSAFUP.....TGNGTLLVVEKHPQLGACT 120  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:.\*  
1: Piri:.\*  
2: Piri:.\*  
3: Piri:.\*  
4: Piri:.\*  
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	116	18.4	132	2 A24402	T-cell receptor al
2	114.5	18.1	136	2 B45893	T-cell receptor al
3	107.5	17.0	138	2 C27577	T-cell receptor al
4	105	16.6	131	2 F45893	T-cell receptor al
5	103	16.3	129	2 A42692	T-cell receptor al
6	102.5	16.2	110	2 B24092	T-cell receptor al
7	101	16.0	120	2 I54487	T-cell receptor al
8	99.5	15.7	131	2 D24092	T-cell receptor al
9	99.5	15.7	131	2 E24092	T-cell receptor al
10	99	15.7	132	1 RWSAV	T-cell receptor al
11	98.5	15.6	130	2 A31211	T-cell receptor al
12	98.5	15.6	146	2 S26408	T-cell receptor al
13	97	15.3	139	2 S36325	T-cell receptor al
14	95.5	15.1	218	2 B47712	myelin/oligodendro
15	95.5	15.1	271	2 A53268	T-cell receptor al
16	94	14.9	526	2 S70587	butyrophilin precu
17	93.5	14.8	247	2 A55717	myelin/oligodendro
18	93	14.7	110	2 A24092	T-cell receptor al
19	93	14.7	117	2 I68824	T-cell receptor al
20	93	14.7	1694	2 S50065	sialoadhesin - mou
21	92.5	14.6	132	2 D45893	T-cell receptor al
22	92.5	14.6	139	2 S36302	T-cell receptor al
23	92.5	14.6	267	1 RWSCH	T-cell receptor al
24	91.5	14.5	107	2 S60590	ig heavy chain var
25	90	14.2	132	2 A27632	T-cell receptor al
26	89	14.1	134	2 A45893	T-cell receptor al
27	88.5	14.0	137	2 C45893	T-cell receptor al
28	88.5	14.0	223	2 A29063	cytotoxic T-lympho
29	88.5	14.0	264	2 F27579	T-cell receptor al

30	88.5	14.0	1197	2 T30581	neural cell adhesi
31	88	13.9	131	2 D44402	T-cell receptor al
32	88	13.9	226	2 A46477	membrane-bound imm
33	88	13.9	946	1 A47299	ror-related recept
34	87.5	13.8	111	2 JH0333	T-cell receptor al
35	87.5	13.8	132	2 S23374	T-cell receptor al
36	87.5	13.8	246	2 A47712	myelin/oligodendro
37	87.5	13.8	247	2 S58394	myelin/oligodendro
38	87	13.8	108	2 JH0342	T-cell receptor al
39	86.5	13.7	95	2 S06003	T-cell receptor al
40	86.5	13.7	129	2 S03478	T-cell receptor al
41	86.5	13.7	874	2 T29548	hypothetical prote
42	86.5	13.7	1273	2 T42405	sax-3 protein - Ca
43	86	13.6	140	2 PHC134	ig lambda chain pr
44	85.5	13.5	134	2 C29774	T-cell receptor al
45	85.5	13.5	223	2 T09536	cytotoxic T-lympho

ALIGNMENTS

RESULT 1  
A24402  
T-cell receptor alpha chain precursor V region (C5) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 23-Aug-1987 #sequence\_revision 23-Aug-1987 #text\_change 30-May-1997  
C:Accession: A24402  
R:Becker, D.M.; Patten, P.; Chien, Y.; Yokota, T.; Eshhar, Z.; Ghedlin, M.; Gascoigne, Nature 317, 430-434, 1995  
A:Title: Variability and repertoire size of T-cell receptor V-alpha gene segments.  
A:Reference number: A93368; MUID:86014379; PMID:2995827  
A:Accession: A24402  
A:Molecule type: mRNA  
A:Residues: 1-132 <BEC>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: T-cell receptor

Query Match 18.4%; Score 116; DB 2; Length 132;  
Best Local Similarity 33.3%; Pred.No. 0.00021;  
Matches 41; Conservative 16; Mismatches 42; Indels 24; Gaps 8;

QY	3	VSQPPE-IRTELGSSAFIPCSFNASQGLAIGSVTWERDEWVPCKEVR-----NGTPE 54
DB	23	VQQSPESLIIVEGANVSLNCSFSDS-----ASQSIWYQQH--PGKGRALISIFSGNKK 76
QY	55	FRGLAPLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVLGLGVGT---GNGTRLVVEK 111
DB	77	-EGRLTVYLNRALEH---VSLHKDSQPSDSAVVLCVARRSGANTGKLTFGHGTLAV-- 130
QY	112	EHP 114
DB	131	-HP 132

RESULT 2  
B45893  
T-cell receptor alpha chain precursor V region (BTA29) - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 20-Jun-2000  
C:Accession: B45893  
R:Ishiguro, N.; Tanaka, A.; Shinagawa, M. Immunogenetics 31, 57-60, 1990  
A:Title: Sequence analysis of bovine T-cell receptor alpha chain.  
A:Reference number: A45893; MUID:90129157; PMID:2137108  
A:Accession: B45893  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-136 <ISH>  
A:Cross-references: GB:P90011; NID:g217610; PIDN:BAAL4061.1; PID:g217611  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: T-cell receptor

Query Match 18.1%; Score 114.5; DB 2; Length 136;

```
Best Local Similarity 29.5%; Pred. No. 0.0003;
Matches 36; Conservative 18; Mismatches 39; Indels 29; Gaps 7;

QY 4 SQPEPTEIRTLGGSAFLPCSFNASQGRLAIGSVTFRDEVPVKGVRNGTPEF----- 55
Db 27 AEPASLPVEGAASLGCTYSNSLY-----FTWYRQ--YFCK-----GPELLQVYANN 75

QY 56 ---RGRPLASSRFLHDHQAELHIRDVRGHDAISYVCRVEVLGLGVGT-----GNGTFLV 108
Db 76 NKEEGKFT--AQSNKTKNH--VSLRIRDSPSDSATYLCVCAVDITSTAGTKLTFGEGTRLI 132

QY 109 VE 110
Db 133 VK 134

RESULT 3
T-cell receptor alpha chain V region (5/10-20D) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 30-May-1997
R/Iwamoto, A.; Ohashi, P.S.; Pirtcher, H.; Walker, C.B.; Michalopoulos, E.E.; Rupp, F.; H.
J. Exp. Med. 165, 591-600, 1987
A/Title: T cell receptor variable gene usage in a specific cytotoxic T cell response. P
A/Reference number: A27557; MUID:87139812; PMID:3493320
A/Accession: C27577
A/Molecule type: mRNA
A/Residues: 1-138 <IWA>
A/Accession: C27557
A/Molecule type: mRNA
A/Residues: 22-138 <IWE>
A/Cross-references: EMBL:X05733
A/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: T-cell receptor

Query Match 17.0%; Score 107.5; DB 2; Length 138;
Best Local Similarity 31.9%; Pred. No. 0.0015;
Matches 38; Conservative 17; Mismatches 45; Indels 19; Gaps 7;

QY 3 VSQPEPTEIRTLGGSAFLPCSFNASQGRLAIGSVTFRDEVPVKGVR-----NGTPE 54
Db 24 VQSPESLIVPEGAMTSLNCTFSDASQY-----FAWYRQH--SGKAPKALMIFNNGEKE 77

QY 55 FRGRPLASSRFLHDHQAELHIRDVRGHDAISYVCRVEVLGLGVGTGNGTFLVVEKE 112
Db 78 -EGRFTHLNKASLH---FSLHIRDQSPSDSALYLCVCAVMTGGYKVVFGSGTRLIVSPD 132

RESULT 4
T-cell receptor alpha chain precursor V region (BTA25) - bovine
C/Species: Bos primigenius taurus (cattle)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 20-Jun-2000
C/Accession: F45893
R/Ishiguro, N.; Tanaka, A.; Shinagawa, M.
Immunogenetics 31, 57-60, 1990
A/Title: Sequence analysis of bovine T-cell receptor alpha chain.
A/Reference number: A45893; MUID:90129157; PMID:2137108
A/Accession: F45893
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-131 <ISH>
A/Cross-references: GB:D90015; NID:G217618; PID:BA44065.1; PID:G217619
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: T-cell receptor
F/36-109/Domain: immunoglobulin homology <IMW>

Query Match 16.6%; Score 105; DB 2; Length 131;
Best Local Similarity 30.3%; Pred. No. 0.0025;
Matches 36; Conservative 23; Mismatches 34; Indels 26; Gaps 8;

QY 3 VSQPEPTEIRTL-EGSSAFLPCSFNASQGRLAIGSVTFRDEVPVKGK-----VRNGTPEF 55
```

```
Db 24 VEQSPSVLSQEGANSTLRCNFSDT-----VDSVQMFQON--PGGALTTLFFIASGTTK- 75
QY 56 RGRPLASSRFLHDHQAELHIRDVRGHDAISYVCRVEVLGLGVGT-----GNGTFLV 109
Db 76 NERMSSTVNSK---ERYSTLHITASQLEDAATYLCVCAVD---LGSNGRQLVFGKGTSLAV 128

RESULT 5
A42692
T-cell receptor alpha chain (lysozyme peptide specific) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C/Accession: A42692
R/Kobori, J.A.; Hood, L.; Shastry, N.
Proc. Natl. Acad. Sci. U.S.A. 89, 2940-2944, 1992
A/Title: Structure-function relationship among T-cell receptors specific for lysozyme pe
A/Reference number: A42692; MUID:92212944; PMID:1313573
A/Accession: A42692
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-129 <KOB>
A/Cross-references: GB:M87844; NID:G201804; PID:AAA51236.1; PID:G554375
A/Experimental source: T-cell hybrid B0H.9.1
A/Note: sequence extracted from NCBI backbone (NCBIN:92850, NCBI:P:92851)
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: T-cell receptor
F/36-109/Domain: immunoglobulin homology <IMW>

Query Match 16.3%; Score 103; DB 2; Length 129;
Best Local Similarity 29.8%; Pred. No. 0.0039;
Matches 39; Conservative 14; Mismatches 34; Indels 44; Gaps 8;

QY 2 WVS-----OPPTEIRTLGGSAFLPCSFNASQGRLAIGSVTFRDE-----VWPG 45
Db 18 WVGDKVKVQSPSALSLOEGTNSALRCNFS-----IAATTQVQFLQNPGRSLINLFYLP- 71

QY 46 KEVRNGTPEPRGLIAPLASSRFLHDHQAELHIRDVRGHDAISYVCRVEVLGLGVGTGN- 103
Db 72 -----GTRKE--NGRLKSAFDSK---ESYSTLHIRDQALEDSDGTFFCAAE-----DTGNYK 116

QY 104 -----GTRLV 109
Db 117 YVFCAGTRLKV 127

RESULT 6
B24092
T-cell receptor alpha chain V region (5C.C7) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 21-Jan-2000
C/Accession: B24092
R/Fink, P.J.; Mattis, L.A.; McElligott, D.L.; Bookman, M.; Hedrick, S.M.
Nature 321, 219-226, 1986
A/Title: Correlations between T-cell specificity and the structure of the antigen recept
A/Reference number: A93380; MUID:86230843; PMID:3012351
A/Accession: B24092
A/Molecule type: mRNA
A/Residues: 1-110 <FIN>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: T-cell receptor
F/16-89/Domain: immunoglobulin homology <IMW>

Query Match 16.2%; Score 102.5; DB 2; Length 110;
Best Local Similarity 31.9%; Pred. No. 0.0037;
Matches 36; Conservative 16; Mismatches 46; Indels 15; Gaps 6;

QY 3 VSQPEPTEIRTL-EGSSAFLPCSFNASQGRLAIGSVTWF-----RDEVPKVRNGTPEFRG 57
Db 4 VEQSPSALSLEHGTSALRCNFTTT-----MRAVQWFRKNSRGSGLINLFYLASGTKE-NG 57

QY 58 RLAPLASSRFLHDHQAELHIRDVRGHDAISYVCRVEVLGLG-VGTGNGTRLV 109
```

Db 58 RLKSAFDSK---ERYSTLHIRDAQLSDSGTYFCAAEASNTNKVFGTGTQLQV 107

## RESULT 7

154487  
T-cell receptor alpha chain - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 09-Jul-2004  
C:Accession: I54487; I68823  
R:Nakajima, P.B.; Di Vincenzo, J.P.; Jameson, S.C.; Gascoigne, N.R.J.  
Immunogenetics 35, 190-198, 1992  
A>Title: Chromosome 14 in B10.A (18R) mice is recombinant and includes Tcr-a alleles.  
A:Reference number: I54487; MUID:92165347; PMID:1371499  
A:Accession: I54487  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-120 <RES>  
A:Cross-references: UNIPROT:Q31213; GB:M55634; NID:G199677; PIDN:AAA39701.1; PID:G199678  
A:Accession: I68823  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 104-120 <RES>  
A:Cross-references: GB:M55634; NID:G199677; PIDN:AAA39702.1; PID:G199679  
A:Note: J-alpha TA61  
C:Genetics:  
A:Gene: MHC-V-alpha-11; J-alpha-TA61  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: transmembrane protein  
P;26-100/Domain: immunoglobulin homology <IMM>

Query Match 16.0%; Score 101; DB 2; Length 120;  
Best Local Similarity 31.6%; Pred. No. 0.0057;  
Matches 36; Conservative 17; Mismatches 47; Indels 14; Gaps 6;

QY 3 VSQPEIRTL-EGSSAFPCSFNASQGLAIGSVTWTFD---EVVPGKEVRNGTPEFRG 57  
Db 14 VEQSPSALSHEGTGSLRCNFTT-----MRSVQFRQNSRGLSLFLYASGTKE-NG 67

QY 58 RLAPLASSRFLHDHQAELHIRDVGRGHDAIYVCRVEVLGVTGNGTRLVVEKEHPOLG 110  
Db 68 RLKSAFDSK---ERYSTLHIRDAQLSDSGTYFCAADNTNTKLTFGDGTVLTVK 119

## RESULT 8

D24092  
T-cell receptor alpha chain precursor V region (B10) - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 19-Nov-1988 #sequence\_revision 01-Dec-2000 #text\_change 11-Jan-2002  
C:Accession: D24092; S03507  
R:Pink, P.J.; Matis, L.A.; McElligott, D.L.; Bookman, M.; Hedrick, S.M.  
Nature 321, 219-226, 1986  
A>Title: Correlations between T-cell specificity and the structure of the antigen receptor  
A:Reference number: A93380; MUID:86230843; PMID:3012351  
A:Accession: D24092  
A:Molecule type: mRNA  
A:Residues: 1-131 <FIN>  
R:Minoco, A.; Mjolsness, S.; Hood, L.  
Nature 316, 832-836, 1995  
A>Title: Genomic organization of the genes encoding mouse T-cell receptor alpha-chain.  
A:Reference number: S03503; MUID:85296332; PMID:2993908  
A:Accession: S03507  
A:Molecule type: DNA  
A:Residues: 111-130 <WIN>  
A:Cross-references: EMBL:G54519; NID:G54519; PIDN:CAA26864.1; PID:G1334131  
A:Note: this sequence was determined from the germline gene  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: T-cell receptor  
F;1-20/Domain: signal sequence #status predicted <SIG>  
F;21-131/Product: T-cell receptor alpha chain V region B10 #status predicted <NAT>  
P;36-109/Domain: immunoglobulin homology <IMM>

Query Match 15.7%; Score 99.5; DB 2; Length 131;  
Best Local Similarity 29.3%; Pred. No. 0.0089;

Matches 36; Conservative 18; Mismatches 42; Indels 27; Gaps 7;  
QY 3 VSQPEIRTL-EGSSAFPCSFNASQGLAIGSVTWTFD---RDEVVPKKEVRNGTPEFRG 57  
Db 24 VEQSPSALSHEGTGSLRCNFTT-----MRAVQWFRKNSRGLSLFLYASGTKE-NG 77  
QY 58 RLAPLASSRFLHDHQAELHIRDVGRGHDAIYVCRVEVLGVTGNGTRLVVEKEHPOLG 117  
Db 78 RLKSAFDSK---ERYSTLHIRDAQLSDSGTYFCAAE-----ATSSGQKLV-----FG 121  
QY 118 AGT 120  
Db 122 QGT 124

## RESULT 9

E24092  
T-cell receptor alpha chain precursor V region (4.C3) - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 21-Jan-2000  
C:Accession: E24092  
R:Pink, P.J.; Matis, L.A.; McElligott, D.L.; Bookman, M.; Hedrick, S.M.  
Nature 321, 219-226, 1986  
A>Title: Correlations between T-cell specificity and the structure of the antigen recep  
A:Reference number: A93380; MUID:86230843; PMID:3012351  
A:Accession: E24092  
A:Molecule type: mRNA  
A:Residues: 1-131 <FIN>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: T-cell receptor  
F;1-20/Domain: signal sequence #status predicted <SIG>  
F;21-131/Product: T-cell receptor alpha chain V region 4.C3 #status predicted <NAT>  
P;36-109/Domain: immunoglobulin homology <IMM>

Query Match 15.7%; Score 99.5; DB 2; Length 131;  
Best Local Similarity 29.3%; Pred. No. 0.0089;

Matches 36; Conservative 18; Mismatches 42; Indels 27; Gaps 7;

QY 3 VSQPEIRTL-EGSSAFPCSFNASQGLAIGSVTWTFD---RDEVVPKKEVRNGTPEFRG 57  
Db 24 VEQSPSALSHEGTGSLRCNFTT-----MRAVQWFRKNSRGLSLFLYASGTKE-NG 77

QY 58 RLAPLASSRFLHDHQAELHIRDVGRGHDAIYVCRVEVLGVTGNGTRLVVEKEHPOLG 117  
Db 78 RLKSAFDSK---ERYSTLHIRDAQLSDSGTYFCAAE-----STSSGQKLV-----FG 121

QY 118 AGT 120  
Db 122 QGT 124

## RESULT 10

RWMSAV  
T-cell receptor alpha chain precursor V region (2B4) - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 28-May-1986 #sequence\_revision 28-May-1986 #text\_change 09-Jul-2004  
C:Accession: A02015  
R:Chien, Y.; Becker, D.M.; Lindsten, T.; Okamura, M.; Cohen, D.I.; Davis, M.M.  
Nature 312, 31-35, 1984  
A>Title: A third type of murine T-cell receptor gene.  
A:Reference number: A93344; MUID:85036634; PMID:6548551  
A:Accession: A02015  
A:Molecule type: mRNA  
A:Residues: 1-132 <CHI>  
A:Cross-references: UNIPROT:P01739  
A:Experimental source: hybridoma 2B4, clone Tt11  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: glycoprotein; heterotetramer; receptor; T-cell  
F;1-20/Domain: signal sequence #status predicted <SIG>  
F;21-132/Product: T-cell receptor alpha chain V region (2B4) #status predicted <NAT>  
F;21-113/Region: V segment  
F;114-117/Region: D segment  
F;118-132/Region: J segment

F;42/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 15.7%; Score 99; DB 1; Length 132;  
 Best Local Similarity 29.4%; Pred. No. 0.01;  
 Matches 37; Conservative 17; Mismatches 42; Indels 30; Gaps 8;

QY 3 VSQPE-IRTEGSSAFPCSFNASQGRLAIGSVTFWRDEVPVQKEVR-----NGTPE 54  
 DB 24 VQSPESLIPEGARTSLNCTFSDASQY-----FWYRQH--SGKAPKALMIFNSGEKE 77

QY 55 FRCLAPLASSRFLHDHQAELHVRGHDASIVYCRVEVLGLGVGTGNGTRLVAVEKEHP 114  
 DB 78 -EGRFTHLKNASH---FSLHVRDQSPDSALYLCAVTLYG-----GSGNKLI----- 122

QY 115 QLGAGT 120  
 DB 123 -FGTGT 127

## RESULT 11

A31211  
 T-cell receptor alpha chain precursor V region (V11.3-J39) - mouse  
 C;Species: Mus musculus (house mouse)  
 C;Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 23-Jul-1999  
 C;Accession: A31211  
 R;Malissen, M.; Trucy, J.; Letourneur, F.; Rebai, N.; Dunn, D.E.; Fitch, F.W.; Hood, L.; Cell 55, 49-59, 1988  
 A;Title: A T cell clone expresses two T cell receptor alpha genes but uses one alpha-beta chain  
 A;Reference number: A94656; MUID:89003051; PMID:3262424  
 A;Accession: A31211  
 A;Molecule type: DNA  
 A;Residues: 1-130 <NAL>  
 A;Cross-references: GB:M22603; NID:G340716; PIDN:AAA63777.1; PID:G710556  
 C;Genetics: 18/1  
 A;Introns: 18/1  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: T-cell receptor  
 F;36-109/Domain: immunoglobulin homology <IMV>

Query Match 15.6%; Score 98.5; DB 2; Length 130;  
 Best Local Similarity 30.6%; Pred. No. 0.011;  
 Matches 35; Conservative 15; Mismatches 42; Indels 29; Gaps 8;

QY 2 WVS-----OPPRTLEGSSAFPCSFNASQGRLAIGSVTFWRDVPVQKEVRN----- 50  
 DB 18 WVGDKVKQSPSALSQEGTNSALRCNFS-----IAATTQVFLQN--PRGSLMNLFLYL 70

QY 51 -GTFEGRGLAPLASSRFLHDHQAELHVRGHDASIVYCRVEVLGLGVGT-----GNGT 105  
 DB 71 PGTK-NGRLKSAFDSK---ESYSLHIRDAQLEDSTGYFCAAG--GGNSGYVQRFGTGT 124

QY 106 RLVV 109  
 DB 125 KLQV 128

## RESULT 12

S26408  
 T-cell receptor beta chain V region (5.5) - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
 C;Accession: S26408  
 R;Bowman, S.J.; Lanchbury, J.S.  
 submitted to the EMBL Data Library, September 1992  
 A;Description: T cell receptor beta chain sequences from patients with rheumatoid arthritis  
 A;Reference number: S26408  
 A;Accession: S26408  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-146 <BOW>  
 A;Cross-references: EMBL:X68527; NID:G36172; PIDN:CAA48540.1; PID:G36173  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: T-cell receptor

F;35-112/Domain: immunoglobulin homology <IMV>

Query Match 15.6%; Score 98.5; DB 2; Length 146;  
 Best Local Similarity 26.0%; Pred. No. 0.013;  
 Matches 33; Conservative 23; Mismatches 44; Indels 27; Gaps 6;

QY 3 VSQPE-IRTEGSSAFPCSFNASQGRLAIGSVTFWRDEVPVQ-----KEYRNGT 52  
 DB 23 VIOQPTHILKT-RQQTVTRCSSQSGH-----NTVSWYQALGGQGFIFQYYREENG- 75

QY 53 PEFRGLAPLASSRFLHDHQAELHVRGHDASIVYCRVEVLGLGVGT-----GNGT 105  
 DB 76 ---RGNPPFRFGLOFPNYSSELNVNALELDDSAVLCASSFKGLGSPRGVQYFGPGT 132

QY 106 RLVVEKE 112  
 DB 133 RLTVTED 139

## RESULT 13

S36325  
 T-cell receptor delta chain precursor - sheep (fragment)  
 C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
 C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 21-Jan-2000  
 C;Accession: S36325; S23040  
 R;Hein, W.R.; Dudley, L.  
 EMBO J. 12, 715-724, 1993  
 A;Title: Divergent evolution of T cell repertoires: extensive diversity and development  
 A;Reference number: S36287; MUID:93178447; PMID:8440261  
 A;Accession: S36325  
 A;Status: preliminary; translation not shown  
 A;Molecule type: mRNA  
 A;Residues: 1-139 <HEI>  
 A;Cross-references: EMBL:Z12997; NID:G2258; PIDN:CAA78341.1; PID:G2259  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: T-cell receptor  
 F;33-113/Domain: immunoglobulin homology <IMV>

Query Match 15.3%; Score 97; DB 2; Length 139;  
 Best Local Similarity 30.6%; Pred. No. 0.017;  
 Matches 37; Conservative 10; Mismatches 52; Indels 22; Gaps 6;

QY 7 PEIITLEGSSAFPCSFNASQGRLAIGSVTFWR---DEVVPGKEVRNGTPEFRGLAPLA 63  
 DB 26 PEQVAVSGREVTLOCTFQTTYSN---PDLYWYKTPDAVQFVLYRDNT---RSRDADFA 79

QY 64 SSRFLHDHQA-----ELHVRGHDASIVYCRVEVLGLGV-----GTGNGTRLVVEK 111  
 DB 80 RGRFTVQHSVRSKTFHLVISSVRPEDTAVYCALD-LQGIYDTDKLTFGKGTRLIVEP 138

QY 112 E 112  
 DB 139 E 139

## RESULT 14

B47712  
 myelin/oligodendrocyte glycoprotein - rat (fragment)  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 21-Jan-1994 #sequence\_revision 30-Apr-1999 #text\_change 09-Jul-2004  
 C;Accession: B47712  
 R;Pham-Dinh, D.; Mattei, M.G.; Nussbaum, J.L.; Rousset, G.; Pontarotti, P.; Roessel, N.; Proc. Natl. Acad. Sci. U.S.A. 90, 7990-7994, 1993  
 A;Title: Myelin/oligodendrocyte glycoprotein is a member of a subset of the immunoglobulin  
 A;Reference number: A47712; MUID:93376728; PMID:8367453  
 A;Accession: B47712  
 A;Status: preliminary; not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 1-218 <PHA>  
 A;Cross-references: UNIPROT:Q63345  
 A;Experimental source: brain  
 A;Note: sequence extracted from NCBI backbone (NCBIP:137804)  
 C;Genetics:

A;Gene: MOG  
C;Function:  
C;Description: may be involved in lipid interaction; may be involved in cell-cell commun  
C;Keywords: glycoprotein; myelin; transmembrane protein  
F;1-218/Product: myelin/oligodendrocyte glycoprotein #status predicted <MAT>  
F;122-150/Domain: transmembrane #status predicted <TM1>  
F;175-200/Domain: transmembrane #status predicted <TM2>  
F;31/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 15.1%; Score 95.5; DB 2; Length 218;  
Best Local Similarity 36.2%; Pred. No. 0.038;  
Matches 34; Conservative 8; Mismatches 33; Indels 19; Gaps 6;

QY 9 IRTLEGSAPLPCSEFNASQGLAIG-SVTWFRDEVVPGKEV-----RNG-----TPERR 56

Db 12 IRLVLGDEALPC--RISPGKATGMEVGWIRS---PFSRVHLRYRNGKDDQDAEQAPEYR 66

QY 57 GRLEAPLASSRFLHDHQAELHIRDVRGHDAIYVC 90

Db 67 GRTELLKES--IGEGKVALRIQNVRFSDGGYTC 98

## RESULT 15

A53268

T-cell receptor alpha chain precursor - sheep

C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C;Date: 02-May-1994 #sequence\_revision 18-Nov-1994 #text\_change 23-Jul-1999

C;Accession: A53268

R;Hein, W.R.; Marcuz, A.; Fichtel, A.; Dudler, L.; Grossberger, D.

Immunogenetics 34, 39-41, 1991

A;Title: Primary structure of the sheep T-cell receptor alpha chain.

A;Reference number: A53268; MUID:91310085; PMID:1830290

A;Accession: A53268

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-271 &lt;HEI&gt;

A;Cross-references: GB:M55622; NID:G166047; PIDN:AAA63518.1; PID:G166048

A;Experimental source: thymus

A;Note: sequence extracted from NCBI backbone (NCBIN:44139, NCBIIP:44140)

C;Superfamily: immunoglobulin C region; immunoglobulin homology

C;Keywords: T-cell receptor

Query Match 15.1%; Score 95.5; DB 2; Length 271;  
Best Local Similarity 30.4%; Pred. No. 0.049;  
Matches 35; Conservative 16; Mismatches 47; Indels 17; Gaps 5;

QY 3 VSOPPE-IRTEGSSAPLPCSEFNASQGLAIGSVTWFRDEVVPGKEV-----RNGTPE 54

Db 23 VSQSPALSVREGDSLVLNCSYTDs---ALYFLQWFRQD--PGKGLISLLSIQANQKEQ 76

QY 55 FGRRLAPLASSRFLHDHQAELHIRDVRGHDAIYVCREVGLGVGTNGTGLVV 109

Db 77 TSGRITVSLDKSRH---SALYIATQSRSDSTTYLCAVTSQGKLVFSGTMLKV 128

Search completed: November 16, 2004, 19:15:51  
Job time : 24.8276 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 16, 2004, 18:56:15 ; Search time 134.005 seconds  
(without alignments)  
515.240 Million cell updates/sec

Title: US-10-036-444-4

Perfect score: 632

Sequence: 1 LWSQPPEIRTELEGSSAFLLP.....TGNGLRVVKEHPQLGACT 120

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 02:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	632	100.0	201	1 NCT3 HUMAN	O14931 homo sapien
2	624	98.7	201	1 NCT3_PANTR	P61484 pan troglod
3	599	94.8	176	1 NCT3_MACFA	P61483 macaca fasc
4	599	94.8	180	1 NCT3_MACMU	C8m102 macaca mula
5	424	67.1	192	1 NCT3_RAT	C8cfd9 rattus norv
6	108.5	17.2	272	2 Q7Q1Q2	Q7q1g2 anopheles g
7	108.5	17.2	449	2 Q9NKA5	Q9nka5 drosophila
8	105.5	16.7	235	2 Q9NM11	Q9nm11 mus musculu
9	103	16.3	329	2 Q8N225	C8n225 homo sapien
10	103	16.3	1340	2 Q8N2A2	C8n2a2 homo sapien
11	102	16.1	172	2 Q71AW3	Q71aw3 bos taurus
12	102	16.1	172	2 AAQ10930	AAQ10930 bos tauru
13	101.5	16.1	221	2 Q28090	Q28090 bos taurus
14	100.5	15.9	221	2 Q97631	Q97631 ovis aries
15	99	15.7	132	1 TVA2 MOUSE	P01739 mus musculu
16	98.5	15.6	273	2 Q6PZF8	C6p2z8 homo sapien
17	98.5	15.6	273	2 AAH5727	AAH5727 homo sapi
18	98	15.5	313	2 Q6IPU1	Q6ipu1 homo sapien
19	98	15.5	313	2 AAH71724	AAH71724 homo sapi
20	97.5	15.4	240	2 Q6MG96	C6mg96 rattus norv
21	97.5	15.4	240	2 CAE83950	CAE83950 rattus no
22	96.5	15.3	350	2 Q9VFU7	Q9vf7 drosophila
23	95.5	15.1	245	1 MCG_RAT	C63345 rattus norv
24	95.5	15.1	245	2 Q6MFX9	C6mfx9 rattus norv
25	95.5	15.1	245	2 CAE84068	CAE84068 rattus no
26	94	14.9	526	1 BUTY HUMAN	Q13410 homo sapien
27	94	14.9	526	2 Q9H458	Q9h458 homo sapien
28	93.5	14.8	246	1 MCG_MOUSE	C61885 mus musculu
29	93.5	14.8	274	2 Q80YU5	C80y45 mus musculu
30	93	14.7	1694	1 SN_MOUSE	C62230 mus musculu
31	92.5	14.6	223	2 Q7TMX1	Q7tmx1 mus musculu

32	92	14.6	174	2	Q9Z1A7	Q9z1a7 rattus norv
33	91.5	14.5	223	2	Q8TT02	Q8tt02 canis famil
34	91.5	14.5	223	2	Q9GKP2	Q9gkp2 canis famil
35	91.5	14.5	223	2	Q62859	Q62859 rattus norv
36	90.5	14.3	272	2	Q70356	Q70356 mus musculu
37	90.5	14.3	600	2	Q7FN36	Q7fn36 anopheles g
38	90	14.2	524	2	Q921K7	Q921k7 mus musculu
39	90	14.2	700	2	Q7TSU7	Q7tsu7 mus musculu
40	90	14.2	700	2	BAC33658	Bac33658 m es cell
41	89.5	14.2	137	2	Q95653	Q95653 homo sapien
42	89	14.1	108	2	Q8CJ25	Q8cj25 orectolobus
43	89	14.1	717	2	Q7PUQ1	Q7puq1 anopheles g
44	88.5	14.0	223	1	CTL4 MOUSE	P09793 mus musculu
45	88.5	14.0	223	2	Q9XSY7	Q9xsy7 felis silve

#### ALIGNMENTS

RESULT 1  
NCT3 HUMAN STANDARD; PRT: 201 AA.  
ID NCT3 HUMAN STANDARD; PRT: 201 AA.  
AC O14931; O14930; O14932; O95667; O95668; O95669;  
DT 05-JUL-2004 (Rel. 44, Created)  
DT 05-JUL-2004 (Rel. 44, Last sequence update)  
DE Natural cytotoxicity triggering receptor 3 precursor (Natural killer cell p30-related protein) (NKP30) (NK-p30).  
GN Name=NCR3; Synonyms=1C7;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 2), TISSUE SPECIFICITY, INTERACTION WITH CD3Z, AND FUNCTION.  
RC TISSUE=Lymphoid;  
RX PubMed=10562324;  
RA Pende D., Parolini S., Pessino A., Sivori S., Augugliaro R., Moretino L., Marcenaro E., Accame L., Malaspina A., Blassoni R., Bottino C., Moretta L., Moretta A.;  
RT "Identification and molecular characterization of NKP30, a novel triggering receptor involved in natural cytotoxicity mediated by human natural killer cells."; J. Exp. Med. 190:1505-1516 (1999).  
RL [2]  
RP SEQUENCE FROM N.A. (ISOFORM 2), TISSUE SPECIFICITY, AND INTERACTION WITH CD3Z.  
RC TISSUE=Peripheral blood;  
RA Sato M., Yabe T., Ohashi J., Tsuchiya N., Hanaoka K., Tokunaga K., Juji T.;  
RT "Identification of two novel single nucleotide polymorphisms in the NKP30 gene in human natural killer cells."; Submitted (FEB-2001) to the EMBL/GenBank/DBSJ databases.  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4; 5 AND 6).  
RX MEDLINE=99219514; PubMed=10202016;  
RA Neville M.J., Campbell R.D.;  
RT "A new member of the Ig superfamily and a V-Atpase G subunit are among the predicted products of novel genes close to the TNF locus in the human MHC."; J. Immunol. 162:4745-4754 (1999).  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
RC TISSUE=Spleen;  
RX MEDLINE=96422187; PubMed=8824804;  
RA Nalabolu S.R., Shukla H., Nallur G., Parimoo S., Weissman S.M.;  
RT "Genes in a 220-Kb region spanning the TNF cluster in human MHC."; Genomics 31:215-222 (1996).  
RN [5]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RX PubMed=14656967; DOI=10.1101/gr.1736803;  
RA Xie T., Rowen L., Aguado B., Ahearn M.E., Madan A., Qin S.,

RA Campbell R.D., Hood L.;  
RT "Analysis of the gene-dense major histocompatibility complex class III  
RL region and its comparison to mouse";  
RN Genome Res. 13:2621-2636(2003).  
[6]  
RP SEQUENCE FROM N.A. (ISOFORM 3).  
RA Shiina S., Tamiya G., Oka A., Inoko H.;  
RT "Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region";  
RL Submitted (G32-1996) to the EMBL/GenBank/DBJ databases.  
[7]  
RN SEQUENCE FROM N.A. (ISOFORM 1).  
RP TISSUE=Blood;  
PC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;  
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshlyki S., Carninci P., Prange C.,  
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc Natl Acad Sci U.S.A. 99:16999-16930(2002).  
CC -!- FUNCTION: Cytotoxicity activating receptor that may contribute to  
CC the increased efficiency of activated natural killer (NK) cells to  
CC mediate tumor cell lysis.  
CC -!- SUBUNIT: Interacts with CD32.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event-Alternative splicing; Named isoforms=6;  
CC Name=1; Synonyms=IC7a;  
CC IsoId=014931-1; Sequence=Displayed;  
CC Note=No experimental confirmation available;  
CC Name=2; Synonyms=IC7c;  
CC IsoId=014931-2; Sequence=VSP\_010413;  
CC Note=No experimental confirmation available;  
CC Name=3; Synonyms=IC7b;  
CC IsoId=014931-3; Sequence=VSP\_010412;  
CC Note=No experimental confirmation available;  
CC Name=4; Synonyms=IC7e;  
CC IsoId=014931-4; Sequence=VSP\_010411;  
CC Note=No experimental confirmation available;  
CC Name=5; Synonyms=IC7f;  
CC IsoId=014931-5; Sequence=VSP\_010411, VSP\_010413;  
CC Note=No experimental confirmation available;  
CC Name=6; Synonyms=IC7d;  
CC IsoId=014931-6; Sequence=VSP\_010412;  
CC Note=No experimental confirmation available;  
CC -!- TISSUE SPECIFICITY: Selectively expressed by all resting and  
CC activated NK cells and weakly expressed in spleen.  
CC -!- SIMILARITY: Belongs to natural cytotoxicity receptor (NCR) family.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; AJ223153; CAB54004.1; -;  
DR EMBL; AB055881; BAB78472.1; -;

DR EMBL; Y14768; CAA75063.1; -;  
DR EMBL; Y14768; CAA75064.1; -;  
DR EMBL; Y14768; CAA75065.1; -;  
DR EMBL; Y14768; CAA75066.1; -;  
DR EMBL; Y14768; CAA75067.1; -;  
DR EMBL; Y14768; CAA75068.1; -;  
DR EMBL; AF031136; AAB86578.1; -;  
DR EMBL; AF031137; AAB86579.1; -;  
DR EMBL; AF031138; AAB86580.1; -;  
DR EMBL; AF123756; AAD18088.1; -;  
DR EMBL; AP000505; BAB63393.1; -;  
DR EMBL; BC052582; AAB52582.1; -;  
DR Genew; HGNC:19077; NCR3.  
DR GO; GO:0006955; P:Immune response; NAS.  
DR GO; GO:0006954; P:Inflammatory response; NAS.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR Pfam; PF00047; IG; 1.  
DR SMART; SM00409; IG; 1.  
DR PROSITE; PS00835; IG LIKE; 1.  
DR Alternative splicing; Glycoprotein; Immunoglobulin domain; Receptor;  
KW Signal; Transmembrane.  
FT SIGNAL 1 18  
FT CHAIN 19 201  
FT DOMAIN 19 135  
FT TRANSMEM 136 156  
FT DOMAIN 157 201  
FT DOMAIN 19 126  
FT DISULFID 39 108  
FT CARBOHYD 42 42  
FT CARBOHYD 121 121  
FT VARSPLIC 66 90  
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FT CLTW

RA TISSUE=Lymphoid;  
RA Biassoni R.;  
RT "Characterization of natural killer receptors in chimpanzees";  
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: Cytotoxicity activating receptor that may contribute to  
CC the increased efficiency of activated natural killer (NK) cells to  
CC mediate tumor cell lysis (By similarity).  
CC -1- SUBUNIT: Interacts with CD3Z (By similarity).  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
CC -1- SIMILARITY: Belongs to natural cytotoxicity receptor (NCR) family.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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CC EMBL; AJ516006; CAD56759.1; -;  
CC DR PROSITE; PS0835; IG LIKE; 1.  
CC KW Glycoprotein; Immunoglobulin domain; Receptor; Signal; Transmembrane.  
CC FT SIGNAL 1 18 Potential.  
CC FT CHAIN 19 201 Natural cytotoxicity triggering receptor  
CC FT DOMAIN 19 135 Extracellular (Potential).  
CC FT TRANSMEM 136 156 Potential.  
CC FT DOMAIN 157 201 Cytoplasmic (Potential).  
CC FT DOMAIN 19 126 IG-like.  
CC FT DISULFID 39 108 By similarity.  
CC FT CARBOHYD 42 42 N-linked (GlcNAc...) (Potential).  
CC FT CARBOHYD 121 121 N-linked (GlcNAc...) (Potential).  
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CC Query Match 98.7%; Score 624; DB 1; Length 201;  
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CC Matches 119; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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CC QY 1 LWSQPEIRTELEGSSAFPCSFNAGQRLAIGSVTFRDEVPVGVKVRNGTPEFRGLA 60  
CC Db 19 LWSQPEIRTELEGSSAFPCSFNAGQRLAIGSVTFRDEVPVGVKVRNETPEFRGLA 78  
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CC Db 79 PLASSRFLHQAEHLHVRDGHDAIYVCRVEVLGVGTGNGTRLVVEKEHPOLGAGT 138  
CC  
CC RESULT 3  
CC NCT3 MACFA STANDARD; PRT; 176 AA.  
CC AC P61483; Q95JB8;  
CC DT 05-JUL-2004 (Rel. 44, Created)  
CC DT 05-JUL-2004 (Rel. 44, Last sequence update)  
CC DT 05-JUL-2004 (Rel. 44, Last annotation update)  
CC DE Natural cytotoxicity triggering receptor 3 precursor (Natural killer  
CC cell p30-related protein) (NKp30) (NK-p30).  
CC GN Name=NCR3;  
CC OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
CC OC Cercopithecoidea; Macaca.  
CC OX NCBI\_TaxID=9541;  
CC [1]  
CC RN SEQUENCE FROM N.A.  
CC RP TISSUE=Lymphoid;  
CC RC Biassoni R.;  
CC RA "Non MHC specific natural cytotoxicity receptors (NCR) expressed in  
CC Macaca fascicularis lymphoid cells";  
CC RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: Cytotoxicity activating receptor that may contribute to  
CC the increased efficiency of activated natural killer (NK) cells to  
CC mediate tumor cell lysis (By similarity).  
CC -----

CC -1- SUBUNIT: Interacts with CD3Z (By similarity).  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
CC -1- SIMILARITY: Belongs to natural cytotoxicity receptor (NCR) family.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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CC EMBL; AJ278389; CAC41081.1; -;  
CC DR HSP; P16410; I185.  
CC DR InterPro; IPR003599; IG.  
CC DR InterPro; IPR007110; IG-like.  
CC DR Pfam; PF00047; IG; 1.  
CC DR SMART; SM00409; IG; 1.  
CC DR PROSITE; PS50835; IG LIKE; 1.  
CC KW Glycoprotein; Immunoglobulin domain; Receptor; Signal; Transmembrane.  
CC FT SIGNAL 1 18 Potential.  
CC FT CHAIN 19 176 Natural cytotoxicity triggering receptor  
CC FT DOMAIN 19 135 Extracellular (Potential).  
CC FT TRANSMEM 136 156 Potential.  
CC FT DOMAIN 157 176 Cytoplasmic (Potential).  
CC FT DOMAIN 19 126 IG-like.  
CC FT DISULFID 39 108 By similarity.  
CC FT CARBOHYD 42 42 N-linked (GlcNAc...) (Potential).  
CC FT CARBOHYD 121 121 N-linked (GlcNAc...) (Potential).  
CC SQ SEQUENCE 176 AA; 19251 MW; 97B2A3B6254AD54 CRC64;  
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CC Best Local Similarity 95.0%; Pred. No. 3.8e-53;  
CC Matches 114; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
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CC Db 79 PLASSRFLHQAEHLHVRDGHDAIYVCRVEVLGVGTGNGTRLVVEKEHPOLGAGT 138  
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CC AC Q8MJ02; Q8MJ00; Q8MJ01; Q95JB8;  
CC DT 05-JUL-2004 (Rel. 44, Created)  
CC DT 05-JUL-2004 (Rel. 44, Last sequence update)  
CC DT 01-OCT-2004 (Rel. 45, Last annotation update)  
CC DE Natural cytotoxicity triggering receptor 3 precursor (Natural killer  
CC cell p30-related protein) (NKp30) (NK-p30).  
CC GN Name=NCR3;  
CC OS Macaca mulatta (Rhesus macaque).  
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
CC OC Cercopithecoidea; Macaca.  
CC OX NCBI\_TaxID=9544;  
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CC RN SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4), AND VARIANT VAL-156.  
CC RP LaBonte M.L., Miller J., Letvin N.L.;  
CC RT "Molecular cloning of rhesus monkey NKp46 and NKp30 and identification  
CC of NKp46SD and NKp30S";  
CC RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: Cytotoxicity activating receptor that may contribute to  
CC the increased efficiency of activated natural killer (NK) cells to  
CC mediate tumor cell lysis (By similarity).  
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RA Caspi A., Tesler G., Pevzner P.A., Hausler D., Roskin K.M.,
RA Baertsch R., Clawson H., Turey T.S., Hinrichs A.S., Karolchik D.,
RA Kent W.J., Rosenbloom K.R., Trumbower H., Weirauch M., Cooper D.N.,
RA Stenson P.D., Ma B., Brent M., Arumugam M., Shneyberg D.,
RA Copley R.R., Taylor M.S., Riethman H., Mudunuri U., Peterson J.,
RA Guyer M., Felsenfeld A., Old S., Mockrin S., Collins F.,
RT "Genomic sequence of the Brown Norway rat yields insights into
RL mammalian evolution.",
RL Nature 428:493-521(2004).
RN [4]
RP IDENTIFICATION.
RX PubMed=15060004; DOI=10.1101/gr.1987704;
RA Hurt P., Walter L., Sudbrak R., Klages S., Mueller I., Shiina T.,
RA Inoko H., Lehrach H., Guenther E., Reinhardt R., Himmelbauer H.,
RT "The genomic sequence and comparative analysis of the rat major
RT histocompatibility complex.",
EL Genome Res. 14:631-639(2004).
CC -!- FUNCTION: Cytotoxicity activating receptor that may contribute to
CC the increased efficiency of activated natural killer (NK) cells to
CC mediate tumor cell lysis (By similarity).
CC -!- SUBUNIT: Interacts with CD32 (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -!- SIMILARITY: Belongs to natural cytotoxicity receptor (NCR) family.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AJ430418; CAD23066.1; -.
CC EMBL; AJ430419; CAD23067.2; -.
CC EMBL; AJ430420; CAD23067.2; JOINED.
CC EMBL; AY273824; AAP13457.1; -.
CC EMBL; BX883046; CA884000.1; -.
CC HSP; P09793; 1DQ7.
CC RGD; 727881; 1C7.
CC InterPro; IPR003599; IG.
CC InterPro; IPR007110; IG-like.
CC Pfam; PF00047; IG; 1.
CC SMART; SM00409; IG; 1.
CC PROSITE; PS0835; IG_LIKE; 1.
KW Glycoprotein; Immunoglobulin domain; Polymorphism; Receptor; Signal;
KW Transmembrane.
FT SIGNAL 1 18 Potential.
FT CHAIN 19 192 Natural cytotoxicity triggering receptor
FT FT
FT DOMAIN 19 147 Extracellular (Potential).
FT TRANSMEM 148 168 Potential.
FT DOMAIN 169 192 Cytoplasmic (Potential).
FT DOMAIN 19 126 IG-like.
FT DISULFID 39 108 By similarity.
FT VARIAT 7 7 I -> V.
FT VARIAT 19 19 I -> V.
FT VARIAT 82 82 A -> V.
FT VARIAT 138 138 A -> T.
FT CONFLICT 135 135 A -> V (in Ref. 2).
SQ SEQUENCE 192 AA; 20470 MW; 7FC84FB252D2377 CRC64;
Query Match 67.1%; Score 424; DB 1; Length 192;
Best Local Similarity 67.8%; Pred. No. 3.4e-35;
Matches 78; Conservative 18; Mismatches 19; Indels 0; Gaps 0;
QY 1 LWSQPEIRTELGSSAFPCSFNAGQRLAIGSVTWFRDEVVPGKEVRNGTEPRGRLA 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
19 IWSQPEIRAQEGTTASLPCSFNAGRAKAAIGSATWQKAPGMELSNVTGPRGRA 78
QY 61 PLASSRLHDHQELHTRDVRGHDASIVYVCRVEVLGLVGTGNGTRLVYKEHPQ 115
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
79 SFSASQFIRHGKAGLLIQDISHDARIYVCRVEVLGLVGTGNGTRLVYKEHPQ 133
```

```
RESULT 6
Q7Q1Q2 PRELIMINARY; PRT; 272 AA.
ID Q7Q1Q2
AC Q7Q1Q2
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE AgCP8128 (Fragment).
DE Names=agCG48749; ORFNames=ENSANGG00000014154;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
RN [1]_TaxID=180454;
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AAAB01008980; EAA14146.1; -.
CC InterPro; IPR007110; IG-like.
CC Pfam; PF00047; IG; 1.
CC PROSITE; PS0835; IG_LIKE; 3.
FT NON_TER 1 1
FT NON_TER 272 272
SQ SEQUENCE 272 AA; 30991 MW; FE1394E3B5C03487 CRC64;
Query Match 17.2%; Score 108.5; DB 2; Length 272;
Best Local Similarity 32.7%; Pred. No. 0.0093;
Matches 32; Conservative 12; Mismatches 37; Indels 17; Gaps 4;
QY 8 EIRTEGSAFLPCSFNAGQRLAIGSVTWFRDEVVPGKEVRNGTEPRGRLA 55
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
9 EIQAVEGRKISLPCLISA-PSGRDKYVMVWTFKDDAGIGLYSFDVRGKPLQARHWSAPEI 67
QY 56 RGRLLAPLASSRFLHDHQELHTRDVRGHDASIVYVCRVE 93
Db 68 FGPRAHFNNTD---TDPATLDIQVRRHDEGVYRCVD 101
RESULT 7
Q9NKA5 PRELIMINARY; PRT; 449 AA.
ID Q9NKA5
AC Q9NKA5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE Hypothetical protein BG:DS01219.3.
DE Name=BG:DS01219.3; ORFNames=CG15275;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=10471707;
RA Ashburner M., Miska S., Roote J., Lewis S.E., Blazej R., Davis T.,
RA Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D.,
RA Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A.,
RA Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitehead K.,
RA Celniker S., Rubin G.M.;
RT "An exploration of the sequence of a 2.9-Mb region of the genome of
RT Drosophila melanogaster: the Adh region.";
RL Genetics 153:179-219(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
```



DT 05-JUL-2004 (FREMURTEL. 27, Last annotation update)

DT 01-NOV-1996 (TFEMBLET. 01, Created)

DT 01-NOV-1996 (TFEMBLET. 01, Created)



DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE CTLA-4 protein precursor.  
GN Name=CTLA-4;  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96186531; PubMed=8606060;  
RA Parsons K.R., Young J.R., Collins R.A., Howard C.J.;  
RT "Cattle CTLA-4, cattle CD28 and chicken CD28 bind human CD86 (B70),  
RL although the MYPPPY hexapeptide is not conserved in cattle CD28.";  
RL Immunogenetics 43:388-391(1996).  
DR EMBL; X93305; CAA63708.1; -.  
DR HSP; P16410; 1185.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR InterPro; IPR008096; CTLA4.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR Pfam; PF00047; Ig; 1.  
DR PRINTS; PR01720; CTLANTIGEN4.  
DR SMART; SM00409; Ig; 1.  
DR PROSITE; PS00835; IG\_LIKE; 1.  
KW Signal.  
FT SIGNAL 1 35 Potential.  
SQ SEQUENCE 221 AA; 24433 MW; 2CAFL48422C597AA CRC64;  
  
Query Match 16.1%; Score 101.5; DB 2; Length 221;  
Best Local Similarity 29.7%; Pred. No. 0.039;  
Matches 35; Conservative 17; Mismatches 59; Indels 7; Gaps 3;  
  
QY 3 VSQPEIRTELGSSAFPCSNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLAPL 62  
Db VTQPPVVLASSRSGVASPCEYESS-GKADEVRTVLKAGIQVTEVCAGTYVVEDELTEL 96  
  
QY 63 ASSEFL---HDHQAEHLHVRGHDASIVYCRVEVL---GLGVGTGNGTGLVVEKEHP 114  
Db DDSTCTGTSRGNKVNLTQGLRAMDTGLYVCKVELMPPPPYVIGNGTQIYVIDPEP 154  
  
RESULT 14  
ID O97631 PRELIMINARY; PRT; 221 AA.  
AC O97631;  
DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Cytotoxic T-lymphocyte-associated protein 4.  
GN Name=CTLA-4;  
OS Ovis aries (Sheep).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Caprinae; Ovis.  
OX NCBI\_TaxID=9940;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=9309828; PubMed=10380709;  
RA Chaplin P.J., Pietrala L.N., Scheerlinck J.P.;  
RT "Cloning and sequence comparison of sheep CD28 and CTLA-4.";  
RL Immunogenetics 49:583-584(1999).  
DR EMBL; AF092740; AAD04380.1; -.  
DR HSP; P16410; 1185.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR InterPro; IPR008096; CTLA4.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR Pfam; PF00047; Ig; 1.  
DR PRINTS; PR01720; CTLANTIGEN4.

DR SMART; SM00409; Ig; 1.  
DR PROSITE; PS00835; IG\_LIKE; 1.  
SQ SEQUENCE 221 AA; 24490 MW; D317E9D5557BA6FB CRC64;  
  
Query Match 15.9%; Score 100.5; DB 2; Length 221;  
Best Local Similarity 28.8%; Pred. No. 0.049;  
Matches 34; Conservative 18; Mismatches 59; Indels 7; Gaps 3;  
  
QY 3 VSQPEIRTELGSSAFPCSNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLAPL 62  
Db VTQPPVVLASSRSGVASPCEYESS-GKADEVRTVLKAGIQVTEVCAGTYVVEDELTEL 96  
  
QY 63 ASSRFL---HDHQAEHLHVRGHDASIVYCRVEVL---GLGVGTGNGTGLVVEKEHP 114  
Db DSSCIGTSRGNKVNLTQGLRAMDTGLYVCKVELMPPPPYVIGNGTQIYVIDPEP 154  
  
RESULT 15  
ID TVA2 MOUSE STANDARD; PRT; 132 AA.  
AC P01739;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE T-cell receptor alpha chain V region 2B4 precursor.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A. (CLONE TT11).  
RX MEDLINE=85036634; PubMed=6548551;  
RA Chien Y., Becker D.M., Lindsten T., Okamura M., Cohen D.I.,  
RA Davis M.M.;  
RT "A third type of murine T-cell receptor gene.";  
RL Nature 312:31-35(1984).  
DR PIR; A02015; RWM5AV.  
DR HSP; P01738; 1TCR.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 1.  
KW Glycoprotein; Immunoglobulin domain; Receptor; Signal; T-cell.  
FT SIGNAL 1 20  
FT CHAIN 21 132 T-cell receptor alpha chain V region 2B4.  
FT DOMAIN 21 113 V segment.  
FT DOMAIN 114 117 D segment.  
FT DOMAIN 118 132 J segment.  
FT CARBOHYD 42 42 N-linked (GlcNAc...).  
FT NON\_TER 132 132  
SQ SEQUENCE 132 AA; 14668 MW; CABBFF6CF1DD3448B CRC64;  
  
Query Match 15.7%; Score 99; DB 1; Length 132;  
Best Local Similarity 29.4%; Pred. No. 0.04;  
Matches 37; Conservative 17; Mismatches 42; Indels 30; Gaps 8;  
  
QY 3 VSQPEIRTELGSSAFPCSNASQGRLAIGSVTWFRDEVVPGKEVR-----NGTPE 54  
Db VQSQPESLIIVPEGARTSLNCTFSDASQY----FWYRQH--SGKAPKALMSIFSNGEKE 77  
  
QY 55 FRGLAPLASSRFLHDHQAEHLHVRGHDASIVYCRVEVLGLGVGTGNGTGLVVEKEHP 114  
Db EGRFTIHLNKASLH---FSLHSDSQPSDLSALFLCAVTLYG-----GSGNKLI----- 122  
  
QY 115 QLQAGT 120  
Db 123 -FGTGT 127  
  
Search completed: November 16, 2004, 19:14:30  
Job time : 135.205 secs



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OM protein - protein search, using sw model  
Run on: November 16, 2004, 17:12:10 ; Search time 127.639 Seconds  
(without alignments)  
337.259 Million cell updates/sec

Title: US-10-036-444-4  
Perfect score: 632  
Sequence: 1 LWSQPPEIRTLGSSAFLP.....TGNQTRLVVEKEHPQLGAGT 120

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 200273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 200273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*  
1: Geneseq1980s:\*  
2: Geneseq1990s:\*  
3: Geneseq2000s:\*  
4: Geneseq2001s:\*  
5: Geneseq2002s:\*  
6: Geneseq2003as:\*  
7: Geneseq2003bs:\*  
8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	632	100.0	120	4	Aae02771 Human Nkp
2	632	100.0	120	8	Adq30924 Human Nkp
3	632	100.0	177	2	Aay06402 Human B-c
4	632	100.0	190	2	Aay06401 Human B-c
5	632	100.0	190	4	Aae02769 Human Nkp
6	632	100.0	190	8	Ado19810 Human PRO
7	632	100.0	190	8	Adq30923 Human Nkp
8	632	100.0	201	2	Aay06403 Human B-c
9	617	97.6	135	5	Aae19109 Human Nkp
10	617	97.6	369	5	Aae19110 Human Nkp
11	607	96.0	382	8	Adp48750 Human Nkp
12	118.5	18.8	139	5	Aau75565 Murine T
13	105.5	16.7	138	4	Aam24182 Rhesus mo
14	105	16.6	140	4	Aab68882 Human REC
15	104	16.5	262	2	Aar97726 B10 singl
16	103	16.3	136	4	Abb11287 Human mem
17	103	16.3	329	7	Adb55555 Human pro
18	103	16.3	3931	6	Abu07377 Human pro
19	103	16.3	3931	7	Adg39786 Human nov
20	101.5	16.1	267	2	Aaw04300 Murine T
21	100.5	15.9	273	7	Adi60192 Secretd
22	99	15.7	246	5	Aae20273 Human lun
23	99	15.7	270	1	Aap50256 Sequence
24	98.5	15.6	252	5	Abp45484 Human Bly
25	98.5	15.6	252	7	Adg96311 Single ch

26	98.5	15.6	740	4	Abc28146	Novel hum
27	97.5	15.4	216	5	Abp58185	CTLA-4-GC
28	96.5	15.3	125	5	Abp52181	Human mon
29	96.5	15.3	350	4	Abb69289	Drosophila
30	95.5	15.1	131	6	Aao29772	Rat myeli
31	95.5	15.1	150	8	Aaw97817	Rat myeli
32	95.5	15.1	218	8	Ado05888	Rat MOP p
33	94	14.9	526	2	Aaw97814	Human but
34	94	14.9	526	5	Aao15804	Human but
35	94	14.9	526	7	Adj69867	Human hea
36	92.5	14.6	235	5	Aag64474	Human typ
37	92.5	14.6	388	5	Abb07681	MOP-Pc fu
38	92.5	14.6	388	6	Ada14265	Mutated M
39	92.5	14.6	388	6	Ada14265	Human imm
40	92	14.6	174	3	Aab08208	Amino aci
41	91.5	14.5	223	2	Aay41083	Canine CT
42	91.5	14.5	268	2	Aar77288	T-cell re
43	91.5	14.5	269	3	Aay69995	Human rec
44	91	14.4	205	2	Aay41173	Llama-Vhh
45	91	14.4	253	5	Abp45534	Human Bly

ALIGNMENTS

RESULT 1  
AAE02771  
ID AAE02771 standard; protein; 120 AA.  
XX  
AC AAE02771;  
XX  
XX 06-AUG-2001 (first entry)  
XX Human Nkp30 receptor extracellular region sequence.  
XX  
XX Human; Nkp30 receptor; natural killer cell; cytostatic; antimicrobial;  
KW melanoma; hepatocarcinoma; lung adenocarcinoma; viral infection; tumour;  
KW immunosuppressant; antiviral; drug; grafting enhancement; leukaemia;  
KW therapy; extracellular region.  
XX  
OS Homo sapiens.  
XX  
XX WO200136630-A2.  
XX  
XX 25-MAY-2001.  
XX  
XX 15-NOV-2000; 2000WO-EP011697.  
XX  
XX 15-NOV-1999; 99CA-02288307.  
XX 15-NOV-1999; 99US-00440514.  
XX  
XX (INNA-) INNATE PHARMA SAS.  
XX (UYGE-) UNIV GENOVA.  
XX  
XX Moretta A, Bottino C, Biassoni R;  
XX WPI; 2001-329221/34.  
XX  
XX Novel compound, useful for detection and/or quantifying the presence of  
XX NK cells, comprises the amino acid sequences of the Nkp30 molecule.  
XX  
XX Claim 1; Fig 7B; 83pp; English.  
XX  
XX The invention relates to human Nkp30 receptor and its corresponding cDNA  
XX molecule which is involved in natural cytotoxicity mediated by natural  
XX killer (NK) cells and antibodies that identify the same. Nkp30 is selected  
XX is a member of immunoglobulin super family (Ig-SF). Nkp30 and its cDNA are  
XX expressed on the surface of human mature NK cells. Nkp30 and its cDNA are  
XX useful for detecting and/or quantifying the presence of NK cells in a  
XX biological sample. The invention also provide kits for detecting and/or  
XX quantifying the presence of NK cells, for the selective removal of NK  
XX cells from a biological sample, for the positive and selective  
XX purification of NK cells from a biological sample and for the in vitro

stimulation of NK cell cytotoxicity. The invention further provides a pharmaceutical composition which is used as a drug for grafting enhancement, graft versus host (GVH) inhibition, stimulation of graft versus tumour (GVT) and especially graft versus leukaemia (GvL), and for the prevention, palliation and/or therapy of solid or liquid tumours, such as melanoma, hepatocarcinoma and lung adenocarcinoma and/or microorganism, notably viral infection. NKp30 antibodies are useful for identifying NKp30 natural ligands and allow assessment of the level of surface NKp30 ligand expressed on an NK-susceptible target cell and the comparison of this level to the standard physiological one. Hence NKp30 antibodies are useful in the diagnosis of tumours or of infection. The present sequence is the extracellular region of human NKp30 receptor

Query Match 100.0%; Score 632; DB 4; Length 120;  
Best Local Similarity 100.0%; Pred. No. 2e-62;  
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LWSQPPPIRTLEGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 60  
DB 1 LWSQPPPIRTLEGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 60

QY 61 PLASRFLHDHQAELHLDVGRGHDASIVYCRVEVLGLGVGTGNGTRLVWEKEHPQLGAGT 120  
DB 61 PLASRFLHDHQAELHLDVGRGHDASIVYCRVEVLGLGVGTGNGTRLVWEKEHPQLGAGT 120

RESULT 2  
ADQ30924  
ID ADQ30924 standard; protein; 120 AA.  
XX AC ADQ30924;  
XX DT 23-SEP-2004 (first entry)  
XX DE Human NKp30 extracellular region.  
XX KW Natural killer cell; NK cell; NKp30; cytostatic; antimicrobial.  
XX OS Homo sapiens.  
XX FN WO2004056392-A1.  
XX PD 08-JUL-2004.  
XX PF 22-DEC-2003; 2003WO-EP014716.  
XX PR 23-DEC-2002; 2002US-0435344P.  
XX PA (INNA-) INNATE PHARMA.  
XX PI Romagne F, Andre P;  
XX DR WPI; 2004-507595/48.  
XX PT Pharmaceutical compositions that stimulate proliferation of natural killer cells useful for therapy of melanoma, chronic myeloid, and leukemia, comprise an anti-natural killer cell receptor antibody and interleukins.  
XX PS Claim 3; SEQ ID NO 2; 35pp; English.  
XX CC The present sequence is that of the extracellular region of human NKp30 ADQ30923, a 190 amino acid polypeptide that is selectively expressed by natural killer (NK) cells, and particularly by mature NK cells. Claimed pharmaceutical compositions that have a stimulating effect on the proliferation of NK cells comprise an antibody such as an anti-NKp30 antibody or anti-NKp46 antibody or its immuno-reactive fragment and a cytokine selected from interleukin-2 (IL2), IL12, IL15 and IL21, the antibody(ies) and cytokine(s) being administered together or separately to a subject. The anti-NKp30 antibody is an isolated antibody or its antigen-binding fragment which specifically binds to NKp30 or to a

fragment, including the extracellular region, of NKp30. The pharmaceutical compositions, when used for daily subcutaneous injection, comprising from 1 mg to 100 mg/kg (body weight) of antibody(ies), and lower than 1 million units/square meter/day of cytokine(s), are useful for the prevention, palliation and therapy of e.g. melanoma, chronic myeloid leukaemia, acute myeloid leukaemia, lymphoma, multiple myeloma, hepatocarcinoma, lung adenocarcinoma, neuroblastoma and for antimicrobial prevention, palliation and therapy (claimed).

QY 1 LWSQPPPIRTLEGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 60  
DB 1 LWSQPPPIRTLEGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 60

QY 61 PLASRFLHDHQAELHLDVGRGHDASIVYCRVEVLGLGVGTGNGTRLVWEKEHPQLGAGT 120  
DB 61 PLASRFLHDHQAELHLDVGRGHDASIVYCRVEVLGLGVGTGNGTRLVWEKEHPQLGAGT 120

RESULT 3  
AA06402  
ID AA06402 standard; protein; 177 AA.  
XX AC AA06402;  
XX DT 20-SEP-1999 (first entry)  
XX DE Human B-cell myelin oligodendrocyte glycoprotein EMOG.  
XX KW MBQG; B-cell myelin oligodendrocyte glycoprotein; human;  
XX KW signal transduction; immunomodulator; antiinflammatory;  
XX KW autoimmune disease; inflammation; gene therapy; diagnosis.  
XX OS Homo sapiens.  
XX FH Key  
XX FT Peptide  
FT Peptide 1..12  
FT Protein /note= "leader peptide"  
FT Modified-site /note= "mature protein"  
FT Modified-site 42  
FT Modified-site /note= "N-glycosylated"  
FT Modified-site 68  
FT Modified-site /note= "N-glycosylated"  
FT Domain /note= "N-glycosylated"  
FT Domain 139..162  
FT Peptide /note= "transmembrane domain"  
FT Peptide 166..177  
FT Peptide /note= "alternatively spliced C-terminal end"  
XX PN WO9223867-A2.  
XX PD 20-MAY-1999.  
XX PF 05-NOV-1998; 98WO-US023826.  
XX PR 07-NOV-1997; 97US-0064761P.  
XX PA (BIOJ ) BIOGEN INC.  
XX PI Browning J;  
XX DR WPI; 1999-418423/35.  
XX DR N-PSDB; AAX59348.  
XX PT Novel B-cell myelin oligodendrocyte glycoproteins.  
XX

PA (BIOJ ) BIOGEN INC.:

```

FT      Region
158.    .190
/label= Intracollulux

```

PA

XX WO200136630-A2.  
 XX 25-MAY-2001.  
 XX 15-NOV-2000; 2000WO-EP011697.  
 XX 15-NOV-1999; 99CA-02288307.  
 XX 15-NOV-1999; 99US-00440514.  
 XX (INNA-) INNATE PHARMA SAS.  
 XX (UYGE-) UNIV GENOVA.  
 XX Moretta A, Bottino C, Biassoni R;  
 XX WPI; 2001-329221/34.  
 XX N-PSDB; AAD06564.  
 XX Novel compound, useful for detection and/or quantifying the presence of  
 XX NK cells, comprises the amino acid sequences of the NKp30 molecule.  
 XX Claim 1; Fig 7B; 83pp; English.  
 XX The invention relates to human NKp30 receptor and its corresponding cDNA  
 XX molecule which is involved in natural cytotoxicity mediated by natural  
 XX killer (NK) cells and antibodies that identify the same. NKp30 receptor  
 XX is a member of immunoglobulin super family (Ig-SF). NKp30 is selectively  
 XX expressed on the surface of human mature NK cells. NKp30 and its cDNA are  
 XX useful for detecting and/or quantifying the presence of NK cells in a  
 XX biological sample. The invention also provide kits for detecting and/or  
 XX quantifying the presence of NK cells, for the selective removal of NK  
 XX cells from a biological sample, for the positive and selective  
 XX purification of NK cells from a biological sample and for the in vitro  
 XX stimulation of NK cell cytotoxicity. The invention further provides a  
 XX pharmaceutical composition which is used as a drug for grafting  
 XX enhancement, graft versus host (GvH) inhibition, stimulation of graft  
 XX versus tumour (GVT), and especially graft versus leukaemia (GvL), and for  
 XX the prevention, palliation and/or therapy of solid or liquid tumours,  
 XX such as melanoma, hepatocarcinoma and lung adenocarcinoma, and/or  
 XX microorganism, notably viral infection. NKp30 antibodies are useful for  
 XX identifying NKp30 natural ligands and allow assessment of the level of  
 XX surface NKp30 ligand expressed on an NK-susceptible target cell and the  
 XX comparison of this level to the standard physiological one. Hence NKp30  
 XX antibodies are useful in the diagnosis of tumours or of infection. The  
 XX present sequence is human NKp30 receptor  
 XX Sequence 190 AA;  
 XX Query Match 100.0%; Score 632; DB 4; Length 190;  
 XX Best Local Similarity 100.0%; Pred. No. 3.6e-62;  
 XX Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LWSQPPIRTLESSAFLPCSFNASQGRLAIGSVTWFRDEVPGKEVRNGTPEFRGLA 60  
 DB 19 LWSQPPIRTLESSAFLPCSFNASQGRLAIGSVTWFRDEVPGKEVRNGTPEFRGLA 78  
 QY 61 PLASSRFLHDHQAEHLHEDVRGHDASIVYCRVEVLGLGVGTGNGTRLVVEKEHPQLGAGT 120  
 DB 79 PLASSRFLHDHQAEHLHEDVRGHDASIVYCRVEVLGLGVGTGNGTRLVVEKEHPQLGAGT 138  
 RESULT 6  
 ID ADO19810  
 XX ADO19810 standard; protein; 190 AA.  
 XX AC ADO19810;  
 XX DT 12-AUG-2004 (first entry)  
 XX DE Human PRO polypeptide #367.  
 XX KW Human; PRO; immune related disorder; systemic lupus erythematosus;  
 XX rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;

KW systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;  
 KW autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;  
 KW diabetes mellitus; renal disease; demyelinating disease;  
 KW central nervous system; peripheral nervous system;  
 KW demyelinating polyneuropathy; Guillain-Barre syndrome;  
 KW chronic inflammatory demyelinating polyneuropathy.  
 XX Homo sapiens.  
 OS WO2004043361-A2.  
 XX 27-MAY-2004.  
 XX 06-NOV-2003; 2003WO-US035268.  
 XX 08-NOV-2002; 2002US-0425235P.  
 XX (GETH ) GENENTECH INC.  
 XX Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;  
 XX Wood WJ, Wu TD;  
 XX WPI; 2004-420067/39.  
 XX N-PSDB; ADO19809.  
 XX Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for  
 XX treating an immune related disorder such as systemic lupus erythematosus,  
 XX rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or  
 XX spondyloarthritis.  
 XX Claim 7; SEQ ID NO 734; 1731pp; English.  
 XX The invention relates to human PRO polypeptides and the polynucleotides  
 XX encoding them. The polypeptides and polynucleotides are useful for  
 XX treating and diagnosing immune related disorders in mammals. The immune  
 XX related disorders include systemic lupus erythematosus, rheumatoid  
 XX arthritis, osteoarthritis, juvenile chronic arthritis, systemic  
 XX sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune  
 XX haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes  
 XX mellitus, immune-mediated renal disease, demyelinating diseases of the  
 XX central or peripheral nervous system, demyelinating polyneuropathy,  
 XX Guillain-Barre syndrome and chronic inflammatory demyelinating  
 XX polyneuropathy. This sequence represents a human PRO polypeptide of the  
 XX invention.  
 XX Sequence 190 AA;  
 XX Query Match 100.0%; Score 632; DB 8; Length 190;  
 XX Best Local Similarity 100.0%; Pred. No. 3.6e-62;  
 XX Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LWSQPPIRTLESSAFLPCSFNASQGRLAIGSVTWFRDEVPGKEVRNGTPEFRGLA 60  
 DB 19 LWSQPPIRTLESSAFLPCSFNASQGRLAIGSVTWFRDEVPGKEVRNGTPEFRGLA 78  
 QY 61 PLASSRFLHDHQAEHLHEDVRGHDASIVYCRVEVLGLGVGTGNGTRLVVEKEHPQLGAGT 120  
 DB 79 PLASSRFLHDHQAEHLHEDVRGHDASIVYCRVEVLGLGVGTGNGTRLVVEKEHPQLGAGT 138  
 RESULT 7  
 ID ADO30923  
 XX ADO30923 standard; protein; 190 AA.  
 XX AC ADO30923;  
 XX DT 23-SEP-2004 (first entry)  
 XX DE Human NKp30 polypeptide.  
 XX KW Natural killer cell; NK cell; NKp30; cytostatic; antimicrobial.  
 XX Homo sapiens.

XX Key Location/Qualifiers  
FH 19..138  
FT /label= Extracellular region  
FT /note= "Region specifically described in Claim 3"  
FT 20..33  
FT /label  
FT /note= "Immunogenic peptide specifically described in Claim 3"  
FT 139..157  
FT /label= Transmembrane region  
FT /note= "Region specifically described in Claim 3"  
FT 158..190  
FT /label= Cytoplasmic tail  
FT /note= "Region specifically described in Claim 3"  
XX WO2004056392-A1.  
XX 08-JUL-2004.  
XX 22-DEC-2003; 2003WO-EP014716.  
XX 23-DEC-2002; 2002US-0435344P.  
XX (INNA-) INNATE PHARMA.  
XX Romagne F, Andre P;  
XX WPI; 2004-507595/48.  
XX Claim 3; SEQ ID NO 1; 35pp; English.  
XX The present sequence is that of human Nkp30, a 190 amino acid polypeptide (about 30 kDa on SDS-PAGE) that is selectively expressed by natural killer (NK) cells, and particularly by mature NK cells. Claimed pharmaceutical compositions that have a stimulating effect on the proliferation of NK cells comprise an antibody such as an anti-Nkp30 antibody or anti-Nkp46 antibody or its immuno-reactive fragment and a cytokine selected from interleukin-2 (IL2), IL12, IL15 and IL21, the antibody(ies) and cytokine(s) being administered together or separately to a subject. The anti-Nkp30 antibody is an isolated antibody or its antigen-binding fragment which specifically binds to Nkp30 or to a fragment ADQ30924-ADQ30927 of Nkp30. The pharmaceutical compositions, when used for daily subcutaneous injection, comprising from 1 ng to 100 mg/kg (body weight) of antibody(ies), and lower than 1 million units/square meters/day of cytokine(s), are useful for the prevention, palliation and therapy of e.g. melanoma, chronic myeloid leukaemia, acute myeloid leukaemia, lymphoma, multiple myeloma, hepatocarcinoma, lung adenocarcinoma, neuroblastoma and for antimicrobial prevention, palliation and therapy (claimed).  
XX Sequence 190 AA;  
Query Match 100.0%; Score 632; DB 8; Length 190;  
Best Local Similarity 100.0%; Pred. No. 3.6e-62;  
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LWVSQPPPIRTLEGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 60  
DB 19 LWVSQPPPIRTLEGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 78  
QY 61 PLASSRFLHDQAEHLIRDVGRGHDASIIYVCRVEVLGVGTGTGTRLWVEKEHPQLGAGT 120  
DB 79 PLASSRFLHDQAEHLIRDVGRGHDASIIYVCRVEVLGVGTGTGTRLWVEKEHPQLGAGT 138  
RESULT 8  
AAY06403

ID AAY06403 standard; protein; 201 AA.  
XX  
AC AAY06403;  
XX  
DT 20-SEP-1999 (first entry)  
XX  
DE Human B-cell myelin oligodendrocyte glycoprotein BMOG.  
XX  
KW BMOG; B-cell myelin oligodendrocyte glycoprotein; human; signal transduction; immunomodulator; antiinflammatory; autoimmune disease; inflammation; gene therapy; diagnosis.  
KW  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH Peptide 1..12  
FT /note= "leader peptide"  
FT Protein 13..201  
FT /note= "mature protein"  
FT Modified-site 42  
FT /note= "N-glycosylated"  
FT Modified-site 68  
FT /note= "N-glycosylated"  
FT Modified-site 121  
FT /note= "N-glycosylated"  
FT Domain 139..162  
FT /note= "transmembrane domain"  
FT Peptide 166..201  
FT /note= "alternatively spliced C-terminal end"  
XX  
XX WO9923867-A2.  
XX 20-MAY-1999.  
XX 05-NOV-1998; 98WO-US023826.  
XX 07-NOV-1997; 97US-0064761P.  
XX (BIOJ ) BIOGEN INC.  
XX Browning J;  
XX WPI; 1999-418423/35.  
XX N-PSDB; AAX59349.  
XX Novel B-cell myelin oligodendrocyte glycoproteins.  
XX Claim 2; Page 43; 43pp; English.  
XX This sequence represents human BMOG, a novel member of the B cell myelin oligodendrocyte glycoprotein family that is expressed by germinal centre B cells. 3 C-terminal splice variants (see AAY06401-03) of BMOG were identified. The protein is present primarily in the spleen, in lymph nodes and in germinal centre B cells. It may have immunoregulatory functions, and soluble or chimeric fusion proteins of BMOG may be used to regulate the immune system in autoimmune or inflammatory diseases. Vectors comprising BMOG, prokaryotic and eukaryotic host cells, and a method of producing BMOG using these transformed host cells are also provided. BMOG polypeptides can be used for modulating the immune system of a subject or to inhibit signal transduction in a cell expressing BMOG by contacting it with a soluble BMOG protein. The nucleic acid can be used for gene therapy. The protein can also be used to target a toxin, imaging agent or radionuclide to a cell expressing BMOG. (All claimed)  
XX Sequence 201 AA;  
Query Match 100.0%; Score 632; DB 2; Length 201;  
Best Local Similarity 100.0%; Pred. No. 3.9e-62;  
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LWVSQPPPIRTLEGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 60  
DB 19 LWVSQPPPIRTLEGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 78

Qy 61 PLASSRFLHDHQAELHLDVRGHDASTYVCRVEVLGVGTGNGTRLVVEKEHPQLGAGT 120  
 DB 79 PLASSRFLHDHQAELHLDVRGHDASTYVCRVEVLGVGTGNGTRLVVEKEHPQLGAGT 138

RESULT 9  
 AAE19109  
 ID AAE19109 standard; protein; 135 AA.  
 AC AAE19109;  
 DT 21-MAY-2002 (first entry)  
 DT 21-MAY-2002 (first entry)  
 DE Human NKp30 protein.  
 KW Human; natural killer cell activating protein; NKp46; therapy; virucide;  
 KW viral infection; natural killer cell; NK; NKp44; imaging agent; cancer;  
 KW detection; carcinoma; melanoma; lymphoma; sarcoma; cytostatic; NKp30.  
 OS Homo sapiens.  
 XX WO200208287-A2.  
 XX 31-JAN-2002.  
 XX 19-JUL-2001; 2001WO-IL000664.  
 XX 20-JUL-2000; 2000IL-00137419.  
 XX (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
 XX (UTNE ) UNIV BEN-GURION NEGEV.  
 XX Mandelboim O, Porgador A;  
 XX WPI; 2002-195870/25.  
 XX N-PSDB; AAD30466.  
 XX New targeting complex capable of targeting an active substance to a  
 XX target cell, comprising a target recognition segment and an active  
 XX segment, useful for treating pathologies associated with viral infections  
 XX or cancer.  
 XX Example 1; Page 108; 113pp; English.  
 XX The invention relates to compositions and methods for the treatment and  
 XX detection of a variety of viral infections, by using complex agents  
 XX comprising the natural killer (NK) cells activating proteins, NKp46 and  
 XX NKp44 and functional fragments thereof, linked to therapeutic or imaging  
 XX agents. The complex is useful for treating pathologies associated with  
 XX viral infections (e.g. infections caused by influenza virus, HIV, Epstein  
 XX -Barr virus, cytomegalovirus, vaccinia virus, ECMV, MVM or herpes virus)  
 XX and cancer (e.g. carcinomas, melanomas, lymphomas and sarcomas), and for  
 XX the imaging and monitoring of cancer. The complex may also be used to  
 XX detect the presence of abnormal cells in a sample. The antibodies can be  
 XX used to qualitatively or quantitatively detect the ligand for the  
 XX complex. The present sequence is human NKp30 protein  
 XX Sequence 135 AA;  
 XX Query Match 97.6%; Score 617; DB 5; Length 135;  
 XX Best Local Similarity 100.0%; Pred. No. 1.1e-60;  
 XX Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LWSQPPPIRTLEGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 60  
 DB 19 LWSQPPPIRTLEGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 78

Qy 61 PLASSRFLHDHQAELHLDVRGHDASTYVCRVEVLGVGTGNGTRLVVEKEHPQLG 117  
 DB 79 PLASSRFLHDHQAELHLDVRGHDASTYVCRVEVLGVGTGNGTRLVVEKEHPQLG 135

RESULT 10  
 AAE19110  
 ID AAE19110 standard; protein; 369 AA.  
 AC AAE19110;  
 DT 29-AUG-2003 (revised)  
 DT 21-MAY-2002 (first entry)  
 DE Human NKp30-IgG fusion protein.  
 KW Human; natural killer cell activating protein; NKp46; therapy; virucide;  
 KW viral infection; natural killer cell; NK; NKp44; imaging agent; cancer;  
 KW detection; carcinoma; melanoma; lymphoma; sarcoma; cytostatic; IgG;  
 KW immunoglobulin G; fusion protein.  
 OS Homo sapiens.  
 OS Chimeric.  
 XX Key Location/Qualifiers  
 XX Region 1..135  
 XX /note= "Human NKp30"  
 XX Region 136..369  
 XX /note= "Human IgG"  
 XX WO200208287-A2.  
 XX 31-JAN-2002.  
 XX 19-JUL-2001; 2001WO-IL000664.  
 XX 20-JUL-2000; 2000IL-00137419.  
 XX (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
 XX (UTNE ) UNIV BEN-GURION NEGEV.  
 XX Mandelboim O, Porgador A;  
 XX WPI; 2002-195870/25.  
 XX N-PSDB; AAD30467.  
 XX New targeting complex capable of targeting an active substance to a  
 XX target cell, comprising a target recognition segment and an active  
 XX segment, useful for treating pathologies associated with viral infections  
 XX or cancer.  
 XX Example 1; Page 108-110; 113pp; English.  
 XX The invention relates to compositions and methods for the treatment and  
 XX detection of a variety of viral infections, by using complex agents  
 XX comprising the natural killer (NK) cells activating proteins, NKp46 and  
 XX NKp44 and functional fragments thereof, linked to therapeutic or imaging  
 XX agents. The complex is useful for treating pathologies associated with  
 XX viral infections (e.g. infections caused by influenza virus, HIV, Epstein  
 XX -Barr virus, cytomegalovirus, vaccinia virus, ECMV, MVM or herpes virus)  
 XX and cancer (e.g. carcinomas, melanomas, lymphomas and sarcomas), and for  
 XX the imaging and monitoring of cancer. The complex may also be used to  
 XX detect the presence of abnormal cells in a sample. The antibodies can be  
 XX used to qualitatively or quantitatively detect the ligand for the  
 XX complex. The present sequence is human NKp30- immunoglobulin G (IgG) Fc  
 XX region fusion protein. (Updated on 29-AUG-2003 to standardise OS field)  
 XX Sequence 369 AA;

Query Match 97.6%; Score 617; DB 5; Length 369;  
 Best Local Similarity 100.0%; Pred. No. 4e-60;  
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LWSQPPPIRTLEGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 60  
 DB 19 LWSQPPPIRTLEGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 78

Qy 61 PLASSRFLHDHQAELHLDVRGHDASTYVCRVEVLGVGTGNGTRLVVEKEHPQLG 117

79 PLASSRFLHDQAEHLHIRDVRGHDSIYVCRVEVLGLGVGTGNGTRLVVEKEHPQLG 135

## RESULT 11

ADP48750  
ID ADP48750 standard; protein; 382 AA.

XX ADP48750;

XX 09-SEP-2004 (first entry)

DE Human NKp30-Fc conjugate protein SEQ ID NO:12.

XX polypeptide conjugate; target recognition; natural killer cell receptor;  
KW cytostatic; gene therapy; neoplastic disease; tumour; carcinoma;  
KW squamous cell carcinoma; adenocarcinoma; small cell carcinoma; melanoma;  
KW glioma; neuroblastoma; B cell lymphoma; T cell lymphoma; leukaemia;  
KW human; natural killer cytotoxicity receptor conjugate;  
KW NKp30-Fc conjugate.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Peptide 1..25

XX Protein 26..382

XX FT /note= "NKp30-Fc conjugate"

XX FT Misc-difference 26..31

XX FT /note= "KpnI site"

XX FT Region 32..148

XX FT /label= NKp30

XX FT Region 149..382

XX FT /label= Fc

XX WO2004053054-A2.

XX 24-JUN-2004.

XX 09-DEC-2003; 2003WO-IL001040.

XX 09-DEC-2002; 2002US-0431728P.

XX (NATS-) NATSPEARS LTD.

XX Mandelboim O, Porgador A;

XX WPI; 2004-468830/44.

XX N-PSDB; ADP48757.

XX New polypeptide conjugate comprising a target recognition segment  
PT comprising a Natural Killer cell receptor consisting of NKp30, useful in  
PT preparing a composition for treating a neoplastic disease.

XX Claim 5; SEQ ID NO 4; 66pp; English.

XX The present invention describes a polypeptide conjugate comprising: (a) a  
CC target recognition segment comprising a natural killer cell receptor  
CC (NCR) or its fragment consisting of NKp30 or its fragment that binds to a  
CC cellular ligand expressed on the surface of a target tumour cell; and (b)  
CC a second segment comprising an active agent capable of exerting a  
CC cytotoxic effect on the target cell. Also described: (1) an isolated  
CC polynucleotide encoding the polypeptide conjugate; (2) a vector  
CC comprising the polynucleotide; (3) a host cell comprising the vector and  
CC capable of expressing the polypeptide conjugate; (4) a pharmaceutical  
CC composition comprising the polypeptide conjugate and a carrier,  
CC stabiliser or diluent; (5) treating a neoplastic disease in a subject;  
CC (6) inhibiting the growth of a tumour in a subject; and (7) delivering a  
CC conjugate substance to a target tumour cell in a subject. The polypeptide  
CC conjugate has cytostatic activity, and can be used in gene therapy. The  
CC polypeptide conjugate is useful in preparing a composition for treating a  
CC neoplastic disease associated with a solid tumour or a non-solid tumour,  
CC e.g., carcinoma, squamous cell carcinomas, adenocarcinomas, small cell

CC carcinomas, melanomas, gliomas, neuroblastomas, B cell lymphoma, T cell  
CC lymphoma or leukaemia. The present sequence represents a human natural  
CC killer cytotoxicity receptor conjugate, designated NKp30-Fc conjugate,  
XX which is used in the exemplification of the present invention.

XX SQ Sequence 382 AA;

Query Match 96.0%; Score 607; DB 8; Length 382;

Best Local Similarity 99.1%; Pred. No. 5.5e-59;

Matches 116; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LWSQPPEIRTLLEGSSAFPLPCSFNASQGRLAIGSVTWFDRDEVVPCKEVRNGTPEFRGLA 60

Db 32 LWSQPPEIRTLLEGSSAFPLPCSFNASQGRLAIGSVTWFDRDEVVPCKEVRNGTPEFRGLA 91

QY 61 PLASSRFLHDQAEHLHIRDVRGHDSIYVCRVEVLGLGVGTGNGTRLVVEKEHPQLG 117

Db 92 PLASSRFLHDQAEHLHIRDVRGHDSIYVCRVEVLGLGVGTGNGTRLVVEKEHPQLG 148

## RESULT 12

AAU75565

ID AAU75565 standard; protein; 139 AA.

XX AC AAU75565;

XX 23-APR-2002 (first entry)

XX Murine T cell receptor beta chain.

XX Immunoglobulin superfamily; GP286; human; immunosuppressive;

XX autoimmune disease; rheumatoid arthritis; cancer; multiple sclerosis;

XX acquired immune deficiency syndrome; AIDS; inflammatory disorder;

XX pancreatitis; antirheumatic; antipsoriatic; dermatological; antianaemic;

XX cytostatic; antileukaemic; antiasthmatic; antiallergic;

XX T cell receptor beta chain.

XX Mus sp.

XX WO200200727-A2.

XX 03-JAN-2002.

XX 22-JUN-2001; 2001WO-US020039.

XX 23-JUN-2000; 2000US-0213630P.

XX 13-APR-2001; 2001US-0283813P.

XX (BIOJ) BIOGEN INC.

XX Carulli JP, Lukashin AV, Kilburn DR, Mathur P;

XX WPI; 2002-090520/12.

XX Isolated polynucleotide encoding a novel human immunoglobulin superfamily  
PT member, named GP286, useful in the treatment of a disease condition that  
PT relates to the immune system, e.g. a transplantation disorder or an  
PT autoimmune disease.

XX Disclosure; Page 167; 180pp; English.

XX The invention relates to an isolated polynucleotide (1) encoding a novel  
CC human immunoglobulin superfamily member, named GP286. The GP286  
CC polynucleotide and polypeptide are useful for the treatment of a disease  
CC condition that relates to the immune system, preferably a disease  
CC autoimmune disease (e.g. rheumatoid arthritis, systemic lupus  
CC erythematosus, psoriasis, Sjogren's syndrome, thyroiditis, Graves'  
CC disease, pulmonary fibrosis, bronchiolitis obliterans, haemolytic anaemia  
CC or Wegener's granulomatosis), cancer (e.g. leukaemia or lymphoma),  
CC multiple sclerosis, graft versus host disease, Kawasaki syndrome,  
CC acquired immune deficiency syndrome (e.g. AIDS) or an inflammatory  
CC disorder (e.g. asthma, allergies, adult respiratory distress syndrome and

CC acute pancreatitis or chronic pancreatitis). The gp286 nucleic acids can  
 CC be used as probes for detecting, characterising and quantifying gp286  
 CC nucleic acids. The present sequence represents the amino acid sequence of  
 CC murine T cell receptor beta chain used in the method of the invention  
 XX  
 SQ Sequence 139 AA;

Query Match 18.8%; Score 118.5; DB 5; Length 139;  
 Best Local Similarity 30.2%; Pred. No. 5.8e-05;  
 Matches 39; Conservative 17; Mismatches 40; Indels 33; Gaps 7;  
 QY 2 WVS-----PPERTLEGSSAFPCSFNASQGLAIGSVTWPERDE-----VWPG 45  
 DB 18 WVSQGVKQPSALQEGTSSALRCNFS-----IATTVQWFLQNSRSLMMLFLVLP- 71  
 QY 46 KEVRNGTPEFRGLRPLASSRFLHDHQAELHIRDVRGHDAIYVCRVEVLGLG--VGTGN 103  
 DB 72 ----GTFKE-NGLKSTFNSK---ESYSTLHIRDAQLEDGTYFCAAEVEGTGSKLSFGK 122  
 QY 104 GTRLVVEKE 112  
 DB 123 GAKLTVSPD 131

RESULT 13  
 AAM24182  
 ID AAM24182 standard; protein; 138 AA.  
 XX  
 AC AAM24182;  
 DT 12-OCT-2001 (first entry)  
 DE Rhesus monkey EST encoded protein SEQ ID NO: 1707.  
 KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;  
 KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;  
 KW diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;  
 KW gene therapy; nutrition.  
 XX  
 OS Macaca mulatta.  
 XX  
 EN WO200154477-A2.  
 XX  
 PD 02-AUG-2001.  
 XX  
 XX 25-JAN-2001; 2001WO-US002687.  
 XX  
 XX 25-JAN-2000; 2000US-00491404.  
 PR 17-JUL-2000; 2000US-00617746.  
 PR 03-AUG-2000; 2000US-00631451.  
 PR 15-SEP-2000; 2000US-00663870.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;  
 PI Cao Y, Drmanac RA, Zhang J, Werhman T;  
 XX  
 WPI: 2001-476164/51.  
 DR N-PSDB; AAM98841.  
 XX  
 PT Isolated polypeptide for treatment of diseases, diagnostics, raising  
 PT antibodies and research use.  
 XX  
 FS Claim 20; Page 1137-1138; 1275pp; English.

XX The present invention provides the protein and coding sequences of novel  
 CC proteins from a variety of organisms, including human, dog, cat, horse,  
 CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea  
 CC urchin and tomato. These were derived from expressed sequence tags (ESTs)  
 CC from the organism of interest. They can be used in diagnostics,  
 CC forensics, gene mapping, identification of mutations, to assess  
 CC biodiversity and for nutritional purposes. The present sequence is a  
 CC protein of the invention

XX Sequence 138 AA;  
 SQ  
 Query Match 16.7%; Score 105.5; DB 4; Length 138;  
 Best Local Similarity 29.1%; Pred. No. 0.0016;  
 Matches 37; Conservative 19; Mismatches 46; Indels 25; Gaps 6;  
 QY 3 VSQPE-IRTEGSSAFPCSFNASQGLAIGSVTWPERDEVVPCKEVRNTPERGLAP 61  
 DB 22 VTQSPALRLQEGESSLNCSTYS-----GLRGUFWYRQD--PGK-----GPEFLFTLYS 70  
 QY 62 LASSR-----FLHDHQAELHIRDVRGHDAIYVCRVEVL-----GLGVGTGNGTRLV 108  
 DB 71 AGEKEKERLKAATYTKESFLHITAPKPEDSATILCAVQAFHSGGADGLTFKGTRLK 130  
 QY 109 VEKEHPQ 115  
 DB 131 VLALYPE 137

RESULT 14  
 AAB68882  
 ID AAB68882 standard; protein; 140 AA.  
 XX  
 AC AAB68882;  
 DT 24-APR-2001 (first entry)  
 DE Human RECAP polypeptide, SEQ ID NO: 12.  
 KW Human; RECAP; receptors and associated proteins; cerebroprotective;  
 KW neotropic; neuroprotective; anticonvulsant; antiparkinsonian; anti-HIV;  
 KW antidiabetic; immunomodulant; immunomodulator; antiinflammatory;  
 KW antithyroid; immunosuppressive; nephrotropic; antigout; thyromimetic;  
 KW cytostatic; antibacterial; viucide; fungicide; protozoacide; cancer.  
 KW antiarteriosclerotic; hepatotropic; gene therapy; infection; cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200107612-A2.  
 XX  
 PD 01-FEB-2001.  
 XX  
 XX 21-JUL-2000; 2000WO-US020035.  
 XX  
 XX 21-JUL-1999; 99US-0145232P.  
 PR 07-OCT-1999; 99US-0158578P.  
 PR 12-NOV-1999; 99US-0165192P.  
 XX  
 PA (INCY-) INCYTE GENOMICS INC.  
 XX  
 PI Au-Young J, Bandman O, Tang YT, Yue H, Azimzai Y, Burford N;  
 PI Baughn MR, Lu DAM, Hillman JL, Patterson C, Lal P;  
 XX  
 WPI: 2001-168554/17.  
 DR N-PSDB; AAF58606.  
 XX  
 PT Novel receptors and associated proteins for diagnosis and treatment of  
 PT neurological disorders, immunological disorders including autoimmune/  
 PT inflammatory disorders and cell proliferative disorders such as cancer.  
 XX  
 PS Claim 1; Page 104; 128pp; English.

XX The present sequence is a human RECAP (receptors and associated proteins)  
 CC polypeptide. RECAP polynucleotides and polypeptides are useful in the  
 CC diagnosis, treatment and prevention of neurological disorders such as  
 CC stroke, Alzheimer's disease, Pick's disease, Huntington's disease,  
 CC dementia, Parkinson's disease, Down's syndrome, amyotrophic lateral  
 CC sclerosis, multiple sclerosis, bacterial and viral meningitis, CJD  
 CC (Creutzfeldt-Jakob disease), GSS (Gerstmann-Strausler-Scheinker  
 CC syndrome); immunological disorders, including autoimmune/inflammatory  
 CC disorders such as AIDS, DiGeorge's syndrome, severe combined  
 CC immunodeficiency disease (SCID), Chediak-Higashi syndrome, Cushing's



CC disease, Addison's disease, autoimmune thyroiditis, Crohn's disease,  
CC diabetes mellitus, Good pasture's syndrome, gout, Grave's disease,  
CC Hashimoto's thyroiditis, Sjogren's syndrome, Werner's syndrome viral,  
CC bacterial, fungal, parasitic, protozoal, and helminthic infections; and  
CC cell proliferation disorders such as arteriosclerosis, atherosclerosis,  
CC cirrhosis, hepatitis and cancer  
XX  
SQ Sequence 140 AA;  
Query Match 16.6%; Score 105; DB 4; Length 140;  
Best Local Similarity 30.3%; Pred. No. 0.0019;  
Matches 36; Conservative 20; Mismatches 37; Indels 26; Gaps 7;  
Qy 3 VSQPE-IRTEGSAFLPCSFNASQGRLAIGSVTFWFRDEWVPGKEVRNGTPEFRGLAP 61  
Db 25 VTQSPALRLQEGESSLNCSTVVS---GLRGLFWYRQD--PGK-----GPEFLTLVS 73  
Qy 62 LASR-----FLHDQALHLDVRGHDASIVYCRVEVLGVGT-----GNGTLLV 109  
Db 74 AGEKEKERLKATLTKEKSFHLHTAPKPEDSASYLCAVQG---GIGNVLHCGSGTQVW 129  
RESULT 15  
AAR97726  
ID AAR97726 standard; protein; 262 AA.  
AC AAR97726;  
XX  
XX 18-SEP-1996 (first entry)  
XX  
XX B10 single chain T-cell receptor.  
XX  
XX Single chain T-cell receptor; TCR; maltose binding protein;  
KW MBP-B10 scTCR; fusion protein; V-alpha; V-beta; antibody; vaccine;  
KW cytochrome-c.  
XX  
XX Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Cleavage-site 6..7 /note= "thrombin cleavage site"  
FT Domain 7..123 /label= V-beta  
FT /note= "residue 8 (Pro in the wild-type) is substituted  
FT by Ser to facilitate thrombin cleavage"  
FT Region 124..150 /label= Linker  
FT Domain 151..256 /label= V-alpha  
FT Domain 257..262 /label= Hexahistidine\_tail  
XX  
FN WO9613593-A2.  
XX  
XX 09-MAY-1996.  
XX  
XX 26-OCT-1995; 95WO-US013770.  
XX  
XX 26-OCT-1994; 94US-00329310.  
XX 01-DEC-1994; 94US-00347893.  
XX 06-JUN-1995; 95US-00468131.  
XX  
XX (PROC-) PROCEPT INC.  
XX  
XX Banerji J, Khandekar S, Bettencourt B, Naylor J, Jones B;  
PI McKeever U, Jesson M, Dwyer D;  
XX  
XX WPI; 1996-239502/24.  
XX N-PSDB; AAT29758.  
XX  
XX New fusion proteins comprising a single chain T-cell receptor - used to  
PT develop prods. for use in detection, diagnosis, functional studies and  
PT therapy involving immune responses.

XX  
PS Example 1; Page 64-65; 104pp; English.  
XX  
CC A soluble single chain T-cell receptor (scTCR) (AAR97726) comprises the V  
CC -beta region of cytochrome c-specific B10 T-cell receptor joined to the  
CC D10 V-alpha region via a linker peptide. It is obtd. by PCR amplification  
CC of V-beta and V-alpha sequences, and cloning into a vector that encodes  
CC the linker. The entire scTCR sequence (AAT29758) is then cloned into  
CC vector pPR998 which encodes maltose binding protein (MBP). The MBP-B10  
CC scTCR fusion protein is expressed in E. coli and purified by affinity  
CC chromatography. Thrombin cleavage yields a soluble scTCR useful in  
CC detection, diagnosis, functional studies and therapy involving immune  
CC responses  
XX  
SQ Sequence 262 AA;  
Query Match 16.5%; Score 104; DB 2; Length 262;  
Best Local Similarity 30.5%; Pred. No. 0.0054;  
Matches 36; Conservative 17; Mismatches 49; Indels 16; Gaps 6;  
Qy 3 VSQPEIRTL-EGSFAFLPCSFNASQGRLAIGSVTFW---RDEVVPGKEVRNGTPEFRG 57  
Db 151 VEQSPSALSLEHGTDLSALRCNFTTT---MRAVQWPKRNSRGSILNLFYLSGTKE-NG 204  
Qy 58 RLAPLASSRFLHDQALHLDVRGHDASIVYCRVEVLGLG--VGTGNGTLLVVEKEH 113  
Db 205 RLKSAFDSK---ERYSTLHIDAQREDSGTYFCAAEATSGOKLVFGQGTILKVYHHH 259  
Search completed: November 16, 2004, 18:55:54  
Job time : 130.639 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2004, 19:14:52 ; Search time 107.268 Seconds  
(without alignments)  
395.815 Million cell updates/sec

Title: US-10-036-444-4

Perfect score: 632

Sequence: 1 LWSVQPPRTLEGSFAFLP.....TGNGRLVVEKEHPQLGAGT 120

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1568699 seqs, 353819137 residues

Total number of hits satisfying chosen parameters: 1568699

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA:\*

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- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	632	100.0	120	13	US-10-036-444-4
2	632	100.0	170	16	US-10-036-259-5
3	632	100.0	190	13	US-10-036-444-2
4	632	100.0	201	16	US-10-036-259-4
5	632	100.0	201	16	US-10-036-259-6
6	617.5	97.7	161	16	US-10-036-259-10
7	617.5	97.6	135	15	US-10-333-481-17
8	617.5	97.5	369	15	US-10-333-481-18
9	603	95.4	175	16	US-10-036-259-8
10	603	95.4	185	16	US-10-036-259-7
11	603	95.4	198	16	US-10-036-259-9
12	118.5	18.8	139	14	US-10-312-495-6
13	107	16.9	1814	16	US-10-367-094-162

14	103	16.3	136	15	US-10-276-774-1657	Sequence 1657, Ap
15	103	16.3	329	14	US-10-104-047-3709	Sequence 3709, Ap
16	103	16.3	3931	14	US-10-120-801-18	Sequence 18, Appl
17	102	16.1	3409	16	US-10-367-094-165	Sequence 165, Appl
18	99	15.7	246	10	US-09-909-567B-49	Sequence 49, Appl
19	98.5	15.6	252	10	US-09-880-748-1495	Sequence 1495, Ap
20	98.5	15.6	252	14	US-10-233-418-1495	Sequence 1495, Ap
21	96.5	15.3	125	16	US-10-432-006-2	Sequence 2, Appl
22	95.5	15.1	218	13	US-10-026-045-1	Sequence 1, Appl
23	94.5	15.0	175	16	US-10-696-259-13	Sequence 13, Appl
24	94	14.9	526	9	US-09-910-174A-9	Sequence 9, Appl
25	94	14.9	526	9	US-09-955-866-13	Sequence 13, Appl
26	94	14.9	526	9	US-09-896-738-19	Sequence 19, Appl
27	94	14.9	526	14	US-10-156-424A-7	Sequence 7, Appl
28	94	14.9	526	16	US-10-408-765A-1673	Sequence 1673, Ap
29	94	14.9	526	16	US-10-644-671-9	Sequence 9, Appl
30	93	14.7	1598	10	US-09-863-776-59	Sequence 59, Appl
31	93	14.7	1694	10	US-09-863-776-57	Sequence 57, Appl
32	92.5	14.6	388	15	US-10-362-591-4	Sequence 4, Appl
33	91.5	14.5	223	16	US-10-790-396-42	Sequence 42, Appl
34	91	14.4	205	9	US-08-252-150-9	Sequence 9, Appl
35	91	14.4	253	10	US-09-880-748-1545	Sequence 1545, Ap
36	91	14.4	253	14	US-10-293-418-1545	Sequence 1545, Ap
37	90.5	14.3	502	14	US-10-363-427-24	Sequence 24, Appl
38	90	14.2	524	15	US-10-042-865-67	Sequence 67, Appl
39	89.5	14.2	110	14	US-10-269-805-50	Sequence 50, Appl
40	89.5	14.2	175	16	US-10-696-259-12	Sequence 12, Appl
41	89.5	14.2	383	10	US-09-898-195A-11	Sequence 11, Appl
42	89.5	14.2	383	14	US-10-057-288-6	Sequence 6, Appl
43	89.5	14.2	383	14	US-10-155-514-10	Sequence 10, Appl
44	89.5	14.2	383	15	US-10-419-008-11	Sequence 11, Appl
45	89	14.1	124	16	US-10-696-259-16	Sequence 16, Appl

#### ALIGNMENTS

#### RESULT 1

US-10-036-444-4  
; Sequence 4, Application US/10036444  
; Publication No. US2002012445A1  
; GENERAL INFORMATION:  
; APPLICANT: INNATE PHARMA S.A.S.  
; TITLE OF INVENTION: "No. US2002012445A1el triggering receptor involved in natural  
; TITLE OF INVENTION: cytotoxicity mediated by human Natural Killer cells and  
; TITLE OF INVENTION: antibodies that identify the same"  
; FILE REFERENCE: SEQ-FR-1660  
; CURRENT APPLICATION NUMBER: US/10/036,444  
; PRIOR FILING DATE: 2002-01-07  
; PRIOR APPLICATION NUMBER: 09/440,514  
; PRIOR FILING DATE: 1999-11-15  
; PRIOR APPLICATION NUMBER: 09/456,199  
; PRIOR FILING DATE: 1999-12-07  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 120  
; TYPE: PRT  
; ORGANISM: Human NK cell  
US-10-036-444-4

Query Match 100.0%; Score 632; DB 13; Length 120;

Best Local Similarity 100.0%; Pred. No. 3.2e-61;

Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	LWSVQPPRTLEGSFAFLP	CSFNASQGRLAIGSVTWFRDEVPCKEVRNGTTPFRGRLA	60
Db	1	LWSVQPPRTLEGSFAFLP	CSFNASQGRLAIGSVTWFRDEVPCKEVRNGTTPFRGRLA	60
Qy	61	PLASSRFLHDHQAELHIRDVGRGHDA	SIYVCRVVLGVGTGNGTRLVVEKEHPOLGAGT	120
Db	61	PLASSRFLHDHQAELHIRDVGRGHDA	SIYVCRVVLGVGTGNGTRLVVEKEHPOLGAGT	120

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19 LWSQPPEIRTLGSSAFPCSFNASQRLAIGSVTWFRDEVPVPGKEVRNGTPEFRGLA 78
61 PLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVLGLGVGTGNGTRLVVKEHPQLGAGT 120
79 PLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVLGLGVGTGNGTRLVVKEHPQLGAGT 138

RESULT 4
US-10-696-259-4
; Sequence 4, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-4

Query Match 100.0%; Score 632; DB 16; Length 190;
Best Local Similarity 100.0%; Pred. No. 5.7e-61;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LWSQPPEIRTLGSSAFPCSFNASQRLAIGSVTWFRDEVPVPGKEVRNGTPEFRGLA 60
DB 19 LWSQPPEIRTLGSSAFPCSFNASQRLAIGSVTWFRDEVPVPGKEVRNGTPEFRGLA 78
QY 61 PLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVLGLGVGTGNGTRLVVKEHPQLGAGT 120
DB 79 PLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVLGLGVGTGNGTRLVVKEHPQLGAGT 138

RESULT 5
US-10-696-259-6
; Sequence 6, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-6

Query Match 100.0%; Score 632; DB 13; Length 190;
Best Local Similarity 100.0%; Pred. No. 5.7e-61;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LWSQPPEIRTLGSSAFPCSFNASQRLAIGSVTWFRDEVPVPGKEVRNGTPEFRGLA 60
DB 19 LWSQPPEIRTLGSSAFPCSFNASQRLAIGSVTWFRDEVPVPGKEVRNGTPEFRGLA 78
QY 61 PLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVLGLGVGTGNGTRLVVKEHPQLGAGT 120
DB 79 PLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVLGLGVGTGNGTRLVVKEHPQLGAGT 138

RESULT 3
US-10-036-444-2
; Sequence 2, Application US/10036444
; Publication No. US20020142445A1
; GENERAL INFORMATION:
; APPLICANT: INNATE PHARMA S.A.S.
; APPLICANT: UNIVERSITA DI GENOVA
; TITLE OF INVENTION: "No. US20020142445A1el triggering receptor involved in natural
; TITLE OF INVENTION: cytotoxicity mediated by human Natural Killer cells and
; TITLE OF INVENTION: antibodies that identify the same"
; FILE REFERENCE: SEQ-PR-1060
; CURRENT APPLICATION NUMBER: US/10/036,444
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 09/440,514
; PRIOR FILING DATE: 1999-11-15
; PRIOR APPLICATION NUMBER: 09/456,199
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Human NK cell
US-10-036-444-2

Query Match 100.0%; Score 632; DB 13; Length 190;
Best Local Similarity 100.0%; Pred. No. 5.7e-61;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LWSQPPEIRTLGSSAFPCSFNASQRLAIGSVTWFRDEVPVPGKEVRNGTPEFRGLA 60
DB 19 LWSQPPEIRTLGSSAFPCSFNASQRLAIGSVTWFRDEVPVPGKEVRNGTPEFRGLA 78
QY 61 PLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVLGLGVGTGNGTRLVVKEHPQLGAGT 120
DB 79 PLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVLGLGVGTGNGTRLVVKEHPQLGAGT 138

RESULT 2
US-10-696-259-5
; Sequence 5, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-5

Query Match 100.0%; Score 632; DB 16; Length 177;
Best Local Similarity 100.0%; Pred. No. 5.2e-61;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LWSQPPEIRTLGSSAFPCSFNASQRLAIGSVTWFRDEVPVPGKEVRNGTPEFRGLA 60
DB 19 LWSQPPEIRTLGSSAFPCSFNASQRLAIGSVTWFRDEVPVPGKEVRNGTPEFRGLA 78
QY 61 PLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVLGLGVGTGNGTRLVVKEHPQLGAGT 120
DB 79 PLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVLGLGVGTGNGTRLVVKEHPQLGAGT 138
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Query Match 100.0%; Score 632; DB 16; Length 201;  
Best Local Similarity 100.0%; Pred. No. 6.1e-61; Indels 0; Gaps 0;  
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LWSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWFDEVPVPGKEVRNGTPEFRGLA 60  
Db 19 LWSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWFDEVPVPGKEVRNGTPEFRGLA 78

Qy 61 PLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTGNGTRLVVEKEHPOLGACT 120  
Db 79 PLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTGNGTRLVVEKEHPOLGACT 138

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US-10-696-259-10  
; Sequence 10, Application US/10696259  
; Publication No. US20040110218A1  
; GENERAL INFORMATION:  
; APPLICANT: BIOGEN, INC  
; APPLICANT: BROWNING, Jeffrey  
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the  
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for  
; TITLE OF INVENTION: Immunomodulatory Purposes  
; FILE REFERENCE: A041 US  
; CURRENT APPLICATION NUMBER: US/10/696,259  
; CURRENT FILING DATE: 2003-10-28  
; PRIOR APPLICATION NUMBER: US/09/560,855A  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: PCT/US98/23826  
; PRIOR FILING DATE: 1998-11-05  
; PRIOR APPLICATION NUMBER: 60/064761  
; PRIOR FILING DATE: 1997-11-07  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 161  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-696-259-10

Query Match 97.7%; Score 617.5; DB 16; Length 161;  
Best Local Similarity 99.2%; Pred. No. 1.9e-59; Indels 1; Gaps 1;  
Matches 119; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 LWSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWFDEVPVPGKEVRNGTPEFRGLA 60  
Db 19 LWSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWFDEVPVPGKEVRNGTPEFRGLA 78

Qy 61 PLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTGNGTRLVVEKEHPOLGACT 120  
Db 79 PLASSRFLHDHQAELHIRDVRGHDASIYVCRVE-LGLGVGTGNGTRLVVEKEHPOLGACT 137

RESULT 7  
US-10-333-481-17  
; Sequence 17, Application US/10333481  
; Publication No. US20040072256A1  
; GENERAL INFORMATION:  
; APPLICANT: Offer Mandelboim  
; APPLICANT: Angel Porgador  
; TITLE OF INVENTION: NK CELLS ACTIVATING RECEPTORS AND THEIR THERAPEUTIC AND DIAGNOSTIC  
; FILE REFERENCE: 68657  
; CURRENT APPLICATION NUMBER: US/10/333,481  
; CURRENT FILING DATE: 2003-08-04  
; PRIOR APPLICATION NUMBER: PCT/IL01/00664  
; PRIOR FILING DATE: 2001-07-19  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 17  
; LENGTH: 135  
; TYPE: PRT  
; ORGANISM: homo sapiens

US-10-333-481-17

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Best Local Similarity 100.0%; Pred. No. 1.6e-59; Indels 0; Gaps 0;  
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LWSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWFDEVPVPGKEVRNGTPEFRGLA 60  
Db 19 LWSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWFDEVPVPGKEVRNGTPEFRGLA 78

Qy 61 PLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTGNGTRLVVEKEHPOLG 117  
Db 79 PLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTGNGTRLVVEKEHPOLG 135

RESULT 8  
US-10-333-481-18  
; Sequence 18, Application US/10333481  
; Publication No. US20040072256A1  
; GENERAL INFORMATION:  
; APPLICANT: Offer Mandelboim  
; APPLICANT: Angel Porgador  
; TITLE OF INVENTION: NK CELLS ACTIVATING RECEPTORS AND THEIR THERAPEUTIC AND DIAGNOSTIC  
; FILE REFERENCE: 68657  
; CURRENT APPLICATION NUMBER: US/10/333,481  
; CURRENT FILING DATE: 2003-08-04  
; PRIOR APPLICATION NUMBER: PCT/IL01/00664  
; PRIOR FILING DATE: 2001-07-19  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 369  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-333-481-18

Query Match 97.6%; Score 617; DB 15; Length 369;  
Best Local Similarity 100.0%; Pred. No. 5.7e-59; Indels 0; Gaps 0;  
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LWSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWFDEVPVPGKEVRNGTPEFRGLA 60  
Db 19 LWSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWFDEVPVPGKEVRNGTPEFRGLA 78

Qy 61 PLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTGNGTRLVVEKEHPOLG 117  
Db 79 PLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTGNGTRLVVEKEHPOLG 135

RESULT 9  
US-10-696-259-8  
; Sequence 8, Application US/10696259  
; Publication No. US20040110218A1  
; GENERAL INFORMATION:  
; APPLICANT: BIOGEN, INC  
; APPLICANT: BROWNING, Jeffrey  
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the  
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for  
; TITLE OF INVENTION: Immunomodulatory Purposes  
; FILE REFERENCE: A041 US  
; CURRENT APPLICATION NUMBER: US/10/696,259  
; CURRENT FILING DATE: 2003-10-28  
; PRIOR APPLICATION NUMBER: US/09/560,855A  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: PCT/US98/23826  
; PRIOR FILING DATE: 1998-11-05  
; PRIOR APPLICATION NUMBER: 60/064761  
; PRIOR FILING DATE: 1997-11-07  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 175  
; TYPE: PRT

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; ORGANISM: Homo sapien
US-10-696-259-8

Query Match          95.4%; Score 603; DB 16; Length 175;
Best Local Similarity 98.3%; Pred. No. 7.8e-58;
Matches 118; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 1 LWSQPPEIRLTGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 60
DB 19 LWSQPPEIRT-EGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 77

QY 61 PLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTGNGTRLVVEKEHPQLGAGT 120
DB 78 PLASSRFLHDHQAELHIRDVRGHDASIYVCRVE-LGLGVGTGNGTRLVVEKEHPQLGAGT 136

RESULT 10
US-10-696-259-7
; Sequence 7, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: ENOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-7

Query Match          95.4%; Score 603; DB 16; Length 185;
Best Local Similarity 98.3%; Pred. No. 8.3e-58;
Matches 118; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 1 LWSQPPEIRLTGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 60
DB 19 LWSQPPEIRT-EGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 77

QY 61 PLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTGNGTRLVVEKEHPQLGAGT 120
DB 78 PLASSRFLHDHQAELHIRDVRGHDASIYVCRVE-LGLGVGTGNGTRLVVEKEHPQLGAGT 136

RESULT 11
US-10-696-259-9
; Sequence 9, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: ENOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05

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; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-9

Query Match          95.4%; Score 603; DB 16; Length 198;
Best Local Similarity 98.3%; Pred. No. 9e-58;
Matches 118; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 1 LWSQPPEIRLTGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 60
DB 19 LWSQPPEIRT-EGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 77

QY 61 PLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTGNGTRLVVEKEHPQLGAGT 120
DB 78 PLASSRFLHDHQAELHIRDVRGHDASIYVCRVE-LGLGVGTGNGTRLVVEKEHPQLGAGT 136

RESULT 12
US-10-312-495-6
; Sequence 6, Application US/10312495
; Publication No. US20030165495A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: A099PCT000454-124
; CURRENT APPLICATION NUMBER: US/10/312,495
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 60/213,630
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/283,813
; PRIOR FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-312-495-6

Query Match          18.8%; Score 118.5; DB 14; Length 139;
Best Local Similarity 30.2%; Pred. No. 7.4e-05;
Matches 39; Conservative 17; Mismatches 40; Indels 33; Gaps 7;

QY 2 WVS-----QPPEIRLTGSSAFPCSFNASQGRLAIGSVTWFRDE-----VVP 45
DB 18 WVSQDVQKQSPSALSLOEGTSSALRCNFS-----IATTVQWFLQNSRGLMNLFLYLP- 71

QY 46 KEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLG--VGTGN 103
DB 72 -----GTKE-NGRLKSTFNK--ESYSTLHIRDAQLEDSTGYFCAAEVGTGSKLSFGK 122

QY 104 GTRLVVEKE 112
DB 123 GAKLTVSPD 131

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RESULT 13
US-10-367-094-162
; Sequence 162, Application US/10367094
; Publication No. US20040170982A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
; FILE REFERENCE: S29452001500
; CURRENT APPLICATION NUMBER: US/10/367,094
; CURRENT FILING DATE: 2003-02-14

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; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 162
; LENGTH: 1814
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-367-094-162

Query Match      16.9%; Score 107; DB 16; Length 1814;
Best Local Similarity 28.7%; Pred. No. 0.032;
Matches 25; Conservative 12; Mismatches 30; Indels 20; Gaps 2;

QY 7 PEIRTLGGSAFLPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLAPLASSR 66
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 818 PDLSTIEGSHALPCTAKGSP-----PAITWCKD-----GHLVSGAEK 857

QY 67 FLHDHQAEHLHIRDVRGHDASIYVCVE 93
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 858 FTLPQSGELLVKNSEGQDAGTYICTAE 884

RESULT 14
US-10-276-774-1657
; Sequence 1657, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 1657
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-276-774-1657

Query Match      16.3%; Score 103; DB 15; Length 136;
Best Local Similarity 28.7%; Pred. No. 0.0036;
Matches 25; Conservative 11; Mismatches 31; Indels 20; Gaps 2;

QY 7 PEIRTLGGSAFLPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLAPLASSR 66
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 32 PDLSTIEGSAFLPCKARGSP-----PNITWCKD-----GQPVSGAEK 71

QY 67 FLHDHQAEHLHIRDVRGHDASIYVCVE 93
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 72 FTLPQSGELLVKNLEGQDAGTYICTAE 98

RESULT 15
US-10-104-047-3709
; Sequence 3709, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3709
; LENGTH: 329
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-3709

Query Match      16.3%; Score 103; DB 14; Length 329;
Best Local Similarity 28.7%; Pred. No. 0.011;
Matches 25; Conservative 11; Mismatches 31; Indels 20; Gaps 2;

QY 7 PEIRTLGGSAFLPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLAPLASSR 66
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 176 PDLSTIEGSAFLPCKARGSP-----PNITWCKD-----GQPVSGAEK 215

QY 67 FLHDHQAEHLHIRDVRGHDASIYVCVE 93
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 216 FTLPQSGELLVKNLEGQDAGTYICTAE 242

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Job time : 108.268 secs
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OM protein - protein search, using sw model

Run on: November 16, 2004, 19:04:36 ; Search time 33.7401 Seconds  
(without alignments)  
235.867 Million cell updates/sec

Title: US-10-036-444-4

Perfect score: 632

Sequence: 1 LKWSQPEIRTEGSSAFPLP.....TNGTRLVVEKHPQLGAGT 120

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

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2: /cgn2\_6/prodata/1/iaa/5B\_COMB.pep:\*  
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4: /cgn2\_6/prodata/1/iaa/5B\_COMB.pep:\*  
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6: /cgn2\_6/prodata/1/iaa/5B\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	101.5	16.1	267	1	US-08-416-336-2
2	99	15.7	270	3	US-09-082-593-10
3	95.5	15.1	218	4	US-10-026-045-1
4	94	14.9	526	4	US-09-910-174B-9
5	94	14.9	526	4	US-09-620-461-9
6	94	14.9	526	4	US-08-724-394A-1
7	92	14.6	174	3	US-08-804-180C-4
8	89.5	14.2	120	3	US-09-171-945-89
9	89.5	14.2	137	3	US-08-804-180C-2
10	89.5	14.2	321	5	PCT-US95-15696-2
11	88	13.9	226	4	US-09-311-784A-32
12	88	13.9	226	4	PCT-US95-08493-13
13	87.5	13.8	120	4	US-09-472-087-102
14	87.5	13.8	187	1	US-08-667-684-14
15	87.5	13.8	187	1	US-08-008-898-14
16	87.5	13.8	187	2	US-08-459-818-14
17	87.5	13.8	187	2	US-08-889-666-14
18	87.5	13.8	187	2	US-08-465-078-14
19	87.5	13.8	187	2	US-08-725-776-14
20	87.5	13.8	187	2	US-08-488-062-14
21	87.5	13.8	187	3	US-08-328-208A-14
22	87.5	13.8	187	4	US-08-253-783-36
23	87.5	13.8	187	5	PCT-US95-06726-36
24	87.5	13.8	218	4	US-10-026-045-3
25	87.5	13.8	223	3	US-08-328-208A-17
26	87.5	13.8	247	5	PCT-US94-10257A-2
27	87.5	13.8	364	4	US-09-472-087-100

Sequence 26, Appl  
Sequence 28, Appl  
Sequence 26, Appl  
Sequence 28, Appl  
Sequence 24, Appl  
Sequence 24, Appl  
Sequence 2, Appl  
Sequence 2, Appl  
Sequence 17, Appl  
Sequence 81, Appl  
Sequence 10, Appl  
Sequence 20, Appl  
Sequence 20, Appl  
Sequence 213, App  
Sequence 213, App  
Sequence 213, App  
Sequence 213, App  
Sequence 79, Appl

#### ALIGNMENTS

RESULT 1  
US-08-416-336-2  
; Sequence 2, Application US/08416336  
; Patent No. 5807714  
; GENERAL INFORMATION:  
; APPLICANT: Ishizaka, Kimishige  
; APPLICANT: Ishii, Yasuyuki  
; TITLE OF INVENTION: METHOD OF PRODUCTION OF ANTIGEN-SPECIFIC  
; TITLE OF INVENTION: GLYCOSYLATION INHIBITING FACTOR  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 4225 Executive Square, Suite 1400  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/416,336  
; FILING DATE: 04-APR-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haile, Lisa H.  
; REGISTRATION NUMBER: 38,347  
; REFERENCE/DOCKET NUMBER: 07246/010001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619/678-5070  
; TELEFAX: 619/678-5099  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 267 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-416-336-2

Query Match  
Best Local Similarity 16.1%; Score 101.5; DB 1; Length 267;  
Matches 38; Conservative 16; Mismatches 39; Indels 33; Gaps 8;  
QY 2 WVS-----QPPEIRTEGSSAFPLPCTGSSQGLAIGSVTWFRDEVVPGKEVRN----- 50  
Db 18 WVSQSKVQSPSALSQEGTNSALRCNFS-----IAATTQVQLQN--PRGSLMNLFLYIV 70  
QY 51 -GTFPRGRLAPLASSRFLHDHQAELHRLDVRGHDASIVYVCVVEVLGIGVGT-----GN 103

Db 71 PGTK-NGRLKSTFNSK-ESYSLHIRDQLEDSGTFFCAAE-----GGGSKYLTFGK 122  
QY 104 GTRLV 109  
Db 123 GTLLTV 128

RESULT 2  
US-09-082-593-10  
; Sequence 10, Application US/09082593  
; Patent No. 6180104  
; GENERAL INFORMATION:  
; APPLICANT: DAVIS, MARK M.  
; APPLICANT: HEDRICK, STEPHEN M.  
; TITLE OF INVENTION: T CELL RECEPTOR BETA SUBUNIT  
; FILE REFERENCE: JX1193-195DIV2  
; CURRENT APPLICATION NUMBER: US/09/082,593  
; CURRENT FILING DATE: 1998-05-20  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 270  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-082-593-10

Query Match 15.7%; Score 99; DB 3; Length 270;  
Best Local Similarity 29.4%; Pred. No. 0.0023;  
Matches 37; Conservative 17; Mismatches 42; Indels 30; Gaps 8;

QY 3 VSQPE-IRTEGSAFLPCSFNASQGLAIGSVTFWFRDEVVPGKEVR-----NGTPE 54  
Db 24 VQSPESLIPEGARTSLNCTFSDASQY----FWYRQH--SGKAPKALMSIFNSGEKE 77  
QY 55 FRGLAPLASSRFLHDHQAELHIRDVRGHDASIYVCVEVLGIGVGTGNGTRLVVEKEHP 114  
Db 78 -EGRFTHLNKASLH---PSLHIRDQPSDSALYLCAVTLYG-----GSGNKLI----- 122  
QY 115 QLGA GT 120  
Db 123 -FETGT 127

RESULT 3  
US-10-026-045-1  
; Sequence 1, Application US/10026045  
; Patent No. 6573236  
; GENERAL INFORMATION:  
; APPLICANT: Genain, Claude P  
; APPLICANT: Hauser, Stephen L  
; TITLE OF INVENTION: Inhibiting MOG-Antibody Binding  
; FILE REFERENCE: UCSF99-020-3  
; CURRENT APPLICATION NUMBER: US/10/026,045  
; CURRENT FILING DATE: 2003-01-13  
; PRIOR APPLICATION NUMBER: US 09/384,036  
; PRIOR FILING DATE: 1999-08-26  
; PRIOR APPLICATION NUMBER: us 60/097,953  
; PRIOR FILING DATE: 1998-08-26  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 218  
; TYPE: PRT  
; ORGANISM: Rattus sp.  
US-10-026-045-1

Query Match 15.1%; Score 95.5; DB 4; Length 218;  
Best Local Similarity 36.2%; Pred. No. 0.0045;  
Matches 34; Conservative 8; Mismatches 33; Indels 19; Gaps 6;

QY 9 IRTLEGSAFLPCSFNASQGLAIG-SVTWFRDEVVPGKEV-----RNG-----TPBFR 56

Db 123 GTLLTV 128

Db 12 IRLVGEAEALPC--RISPGKNATGMEVGYRS---PFSRVVHLRYNGKQDQAEQAPEYR 66  
QY 57 GRPLAPLASSRFLHDHQAELHIRDVRGHDASIYVC 90  
Db 67 GRTELLKES--IGEGKVALRIQNVRFSDGGGYTC 98

RESULT 4  
US-09-910-174B-9  
; Sequence 9, Application US/09910174B  
; Patent No. 6630575  
; GENERAL INFORMATION:  
; APPLICANT: Coyle, Anthony J.  
; APPLICANT: Fraser, Christopher C.  
; APPLICANT: Manning, Stephen  
; TITLE OF INVENTION: B7-H2 Molecules, No. 6630575el Members of the B7  
; FILE REFERENCE: 35800/236924  
; CURRENT APPLICATION NUMBER: US/09/910,174B  
; CURRENT FILING DATE: 2001-07-20  
; PRIOR APPLICATION NUMBER: US 09/620,461  
; PRIOR FILING DATE: 2000-07-20  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 526  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-910-174B-9

Query Match 14.9%; Score 94; DB 4; Length 526;  
Best Local Similarity 39.6%; Pred. No. 0.021;  
Matches 38; Conservative 5; Mismatches 37; Indels 16; Gaps 7;

QY 6 PPE-IRTEGSAFLPC--SFNASQGLAIGSVTFWFRDEVVPGKEV-RNG-----TPE 54  
Db 34 PPEPILAVVGDEALPCRLSPNASEHL---ELRWFRKKVSPAVLVHRDGRGEAEQMP 90  
QY 55 FRGLAPLASSRFLHDHQAELHIRDVRGHDASIYVC 90  
Db 91 YRGR-ATLVQDGIAGRVA-LRINGVRVSDGGEYTC 124

RESULT 5  
US-09-620-461-9  
; Sequence 9, Application US/09620461  
; Patent No. 6635750  
; GENERAL INFORMATION:  
; APPLICANT: Coyle, Anthony J.  
; APPLICANT: Fraser, Christopher C.  
; APPLICANT: Manning, Stephen  
; TITLE OF INVENTION: B7-H2 Molecules, No. 6635750el Members of the B7  
; FILE REFERENCE: 5800-149  
; CURRENT APPLICATION NUMBER: US/09/620,461  
; CURRENT FILING DATE: 2000-07-20  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 9  
; LENGTH: 526  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-620-461-9

Query Match 14.9%; Score 94; DB 4; Length 526;  
Best Local Similarity 39.6%; Pred. No. 0.021;  
Matches 38; Conservative 5; Mismatches 37; Indels 16; Gaps 7;

QY 6 PPE-IRTEGSAFLPC--SFNASQGLAIGSVTFWFRDEVVPGKEV-RNG-----TPE 54  
Db 34 PPEPILAVVGDEALPCRLSPNASEHL---ELRWFRKKVSPAVLVHRDGRGEAEQMP 90  
QY 55 FRGLAPLASSRFLHDHQAELHIRDVRGHDASIYVC 90

Db 91 YRGR-ATLVQDGIAGKGRVA-LRIRGVRVSDGGEYTC 124

RESULT 6  
US-08-724-394A-1  
; Sequence 1, Application US/08724394A  
; Patent No. 5872237  
; GENERAL INFORMATION:  
; APPLICANT: Feder, John N.  
; APPLICANT: Kronmal, Gregory S.  
; APPLICANT: Lauer, Peter M.  
; APPLICANT: Ruddy, David A.  
; APPLICANT: Thomas, Winston  
; APPLICANT: Tsuchihashi, Zenta  
; APPLICANT: Wolff, Roger K.  
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el  
; TITLE OF INVENTION: Sequences and Antibodies Thereto  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/724,394A  
; FILING DATE: 01-OCT-1996  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fitts, Renee A.  
; REGISTRATION NUMBER: 35,136  
; REFERENCE/DOCKET NUMBER: 017957-000100  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-576-0200  
; TELEFAX: 415-576-0300  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 589 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: not relevant  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Region  
; LOCATION: 1-589  
; OTHER INFORMATION: /note= "BT"

US-08-724-394A-1

Query Match 14.9%; Score 94; DB 2; Length 589;

Best Local Similarity 39.6%; Pred. No. 0.025;

Matches 38; Conservative 5; Mismatches 37; Indels 16; Gaps 7;

QY 6 PPE-INTLEGGSAFLPC-SFNASQGRLAIGSVTWRDEVPCKEV-RNG-----TPE 54

Db 37 PPEPILAVVGDEAELFCRLSPNASEHL---ELRWFVKVSPAVLVRDGRGEQAEQMP 93

QY 55 FRGLAPLASSRFLHDQAEHLHVRGHDASIYVC 90

Db 94 YRGR-ATLVQDGIAGKGRVA-LRIRGVRVSDGGEYTC 127

RESULT 7

US-08-804-180C-4

; Sequence 4, Application US/08804180C

; Patent No. 6107056

; GENERAL INFORMATION:

; APPLICANT: Emery, Stephen

; APPLICANT: Copley, Clive Graham

; APPLICANT: Edge, Michael Derek

; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said

; TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System

; APPLICANT: Martin K. Oaks  
; TITLE OF INVENTION: sCTLA-4 and Its Soluble Products  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Thomas M. Wozny  
; STREET: 100 East Wisconsin Avenue  
; CITY: Milwaukee  
; STATE: Wisconsin  
; COUNTRY: USA  
; ZIP: 53202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.50 inch Disk  
; COMPUTER: IBM  
; OPERATING SYSTEM: DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/804,180C  
; FILING DATE: February 20, 1997  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Thomas M. Wozny  
; REGISTRATION NUMBER: 28,922  
; REFERENCE/DOCKET NUMBER: 3284-00003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (414) 271-7590  
; TELEFAX: (414) 271-5770  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 174  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: Polypeptide  
; DESCRIPTION: Internal fragment  
; HYPOTHETICAL: no  
; FRAGMENT TYPE: Internal fragment  
; ORIGINAL SOURCE:  
; ORGANISM: Rattus No. 6107056vegicus  
; STRAIN: ACI  
; DEVELOPMENTAL STAGE: Adult  
; CELL TYPE: Splenocyte  
; FEATURE:  
; NAME/KEY: Rat sCTLA-4  
; IDENTIFICATION METHOD: Found by experiment  
; OTHER INFORMATION: B7 binding protein  
; US-08-804-180C-4

Query Match 14.6%; Score 92; DB 3; Length 174;

Best Local Similarity 29.5%; Pred. No. 0.0085;

Matches 36; Conservative 19; Mismatches 49; Indels 18; Gaps 7;

QY 3 VSQPEIRTLGSSAFLPC---SFNASQGRLAIGSVTWRDEVPCKEVNGTPEFRGR 58

Db 40 VTQPSVVLASSHGVSAPFCEYASSHNTDEVTVLRQT--NDQVT---EVCATFTVKNT 94

QY 59 LA----PLASSRFLHDQAEHLHVRGHDASIYVCVEVL---GLGVGTGNGTRL-VVE 110

Db 95 LGFLDDPFCSCGTF-NESRVNLTIOQLRAADTGLYFCVKELMYPPEYVGMGNGTQIVIA 153

QY 111 KE 112

Db 154 KE 155

RESULT 8

US-09-171-945-89

; Sequence 89, Application US/09171945

; Patent No. 6277599

; GENERAL INFORMATION:

; APPLICANT: Emery, Stephen

; APPLICANT: Copley, Clive Graham

; APPLICANT: Edge, Michael Derek

; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said

; TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System

```
; FILE REFERENCE: Monoclonal Antibody to CEA
; CURRENT APPLICATION NUMBER: US/09/171,945
; CURRENT FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: GB9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 89
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: humanized
; US-09-171-945-89

Query Match          14.2%; Score 89.5; DB 3; Length 120;
Best Local Similarity 27.8%; Pred. No. 0.01;
Matches 32; Conservative 10; Mismatches 34; Indels 39; Gaps 6;

QY 2 WVSQPPEIRLTGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNG---TPERRG 57
Db 36 WVRQPP-----GR-GLGWIGWIDPE-----NGDTYAPKFRG 66

QY 58 RLAPLASSRFLPHQAEHLHVRGHDASIYVCRVEVLGLGVGT---GNGTRLVV 109
Db 67 RATWLADS---SKNQASRLSSVTAADTAVYCHVLIYAGYLANDYWGQGLTVTV 118

RESULT 9
US-08-804-180C-2
; Sequence 2, Application US/08804180C
; Patent No. 6107056
; GENERAL INFORMATION:
; APPLICANT: Martin K. Oaks
; TITLE OF INVENTION: sCTLA-4 and Its Soluble Products
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Thomas M. Wozny
; STREET: 100 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.50 inch Disk
; COMPUTER: IBM
; OPERATING SYSTEM: DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/804,180C
; FILING DATE: February 20, 1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas M. Wozny
; REGISTRATION NUMBER: 28,922
; REFERENCE/DOCKET NUMBER: 3284-00003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 271-7590
; TELEFAX: (414) 271-5770
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 137
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; DESCRIPTION: no
; HYPOTHETICAL: no
; FRAGMENT TYPE: Mature Polypeptide
; ORIGINAL SOURCE:
```

```
; ORGANISM: Homo Sapien
; DEVELOPMENTAL STAGE: Adult
; TISSUE TYPE: Lymphnode
; FEATURE:
; NAME/KEY: Human sCTLA-4
; IDENTIFICATION METHOD: Found by experiment
; OTHER INFORMATION: Asn 76 and Asn 108 represent N-linked glycosylation; B7 bindi
US-08-804-180C-2

Query Match          14.2%; Score 89.5; DB 3; Length 137;
Best Local Similarity 25.2%; Pred. No. 0.012;
Matches 33; Conservative 18; Mismatches 59; Indels 21; Gaps 4;

QY 3 VSQPPEIRLTGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLIAPL 62
Db 3 VAQPAVVLASSRGIAISFVCEY-ASPGKATEVRVTILRQADSQVTEVCAATYMMGNELT-- 59
QY 63 ASSRFLHD-----HQAELHVRDVRGHDASIYVCRVEVL-----GLGVGTGNGTRLV 108
Db 60 ----FLDDSTCTGTSSGNQVNLTIQGRAMDGLYICKVELMYPPPYLIGNGTQIYVI 115
QY 109 VEKEHPOLGAG 119
Db 116 AKKKPSYNRG 126

RESULT 10
PCT-US95-15696-2
; Sequence 2, Application PC/TUS9515696
; GENERAL INFORMATION:
; APPLICANT: President and Fellows of Harvard College
; TITLE OF INVENTION: SINGLE CHAIN T-CELL RECEPTOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kevin M. Farrell, P.C.
; STREET: P.O. Box 999
; CITY: York Harbor
; STATE: Maine
; COUNTRY: USA
; ZIP: 03911
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/15696
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/349,915
; FILING DATE: 06-DEC-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Farrell, Kevin M.
; REGISTRATION NUMBER: 35,505
; REFERENCE/DOCKET NUMBER: HU-9404 WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 207-363-0558
; TELEFAX: 207-363-0528
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 391 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-15696-2

Query Match          14.2%; Score 89.5; DB 5; Length 391;
Best Local Similarity 27.6%; Pred. No. 0.048;
Matches 34; Conservative 17; Mismatches 49; Indels 23; Gaps 7;

QY 6 PPEIRLTGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEV-----RNGTPEFRGR 58
```

```
Db 31 PQALSTQEGENATWNSYKTS-----INLQWTRQN--SGRGLVHLILIRSNREKHSR 83
QY 59 L-APLASSRFLDHQAEHLHVRGHDASIYVCRVFLGLGVGT-NGTRLVVEKEHPQL 116
Db 84 LRVTLDTSK---KSSSLLITARAADTASYFCATDGTGGSYIPTFGRTSLIV---HPSS 136
QY 117 GAG 119
Db 137 GGG 139

RESULT 11
US-09-311-784A-32
; Sequence 32, Application US/09311784A
; Patent No. 6534482
; GENERAL INFORMATION:
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE REFERENCE: 39963-20022.01
; CURRENT APPLICATION NUMBER: US/09/311,784A
; PRIOR FILING DATE: 1999-05-13
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human MB-1 Ig-alpha
US-09-311-784A-32

Query Match 13.9%; Score 88; DB 4; Length 226;
Best Local Similarity 29.9%; Pred. No. 0.035;
Matches 38; Conservative 13; Mismatches 50; Indels 26; Gaps 7;

QY 1 LMTVSQ-PPEIRTLGSSAFPLPCSNASQGRLAIGSVTWRDEVPVPGKEVNGT--PEFRG 57
Db 33 LWMHKVPASLMVSLGEDAHFQCPHNSNN-----ANVTWR--VLHG---NYTWPEFLG 82
QY 58 RLAPLASSRFLDHQAEHLHVRGHDASIYVCRVFLGLGVGTNGTRLVVEKEHPQ-- 115
Db 83 P-----GEDPNGTLTIQNVKGGHGIYVCRVQEGNESYQQSCGTLYRVRPQPPRPF 133
QY 116 --LGAGT 120
Db 134 LDMGEGT 140

RESULT 12
PCT-US95-08493-13
; Sequence 13, Application PC/TUS9508493
; GENERAL INFORMATION:
; APPLICANT: Wood, Clive
; APPLICANT: Caruso, Anthony
; TITLE OF INVENTION: Novel mlk Receptor Tyrosine Kinases
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LEGAL AFFAIRS
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08493
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: GI5234A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 498-8224
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 946 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-08493-13

Query Match 13.9%; Score 88; DB 5; Length 946;
Best Local Similarity 29.3%; Pred. No. 0.23;
Matches 27; Conservative 13; Mismatches 24; Indels 28; Gaps 5;

QY 3 VSQPEIRTLGSSAFPLPCSNASQGRLAIG-----SVTWRDEVPVPGKEVNGTPEFRGR 58
Db 126 IRPPTDVRALLGSKVLPCS-----TMGNPKPAISWFKDETA----LKNDQF----R 169
QY 59 LAPLASSRFLDHQAEHLHVRGHDASIYVC 90
Db 170 TSVLES-----GNLRNVQLEDAGKYRC 193

RESULT 13
US-09-472-087-102
; Sequence 102, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, BILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR FILING DATE: 1999-12-23
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 102
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-102

Query Match 13.8%; Score 87.5; DB 4; Length 120;
Best Local Similarity 27.4%; Pred. No. 0.017;
Matches 34; Conservative 15; Mismatches 56; Indels 19; Gaps 4;

QY 3 VSQPEIRTLGSSAFPLPCSNASQGRLAIGSVTWRDEVPVPGKEVNGTPEFRGLAPL 62
Db 3 VAQPAVVLASSRGIASFVCEY-ASPGRATEVRVTVLROADSQVTEVCAATVMGNELT-- 59
QY 63 ASSRFLHD-----HQAELHVRGHDASIYVCRVEYL---GLGVGTGNGTRLVWE 110
```

Db 60 -----FLDDSICTSGNQVNLTIQGLRANDTGLYICKVELMYPYPYLGNGTQIYVI 115

Qy 111 KEHP 114

Db 116 DPEP 119

## RESULT 14

US-08-067-684-14  
; Sequence 14, Application US/08067684  
; Patent No. 5434131  
; GENERAL INFORMATION:  
; APPLICANT: Linsley, Peter S.  
; APPLICANT: Ledbetter, Jeffrey A.  
; APPLICANT: Damle, Nitin K.  
; APPLICANT: Brady, William  
; TITLE OF INVENTION: CTLA4 RECEPTOR AND METHODS FOR ITS USE  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sheldon & Mak  
; STREET: 225 South Lake Avenue, Suite 900  
; CITY: Pasadena  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 91101

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/067,684  
; FILING DATE: 26-MAY-1993  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Adriano, Sarah B.  
; REGISTRATION NUMBER: 34,470  
; REFERENCE/DOCKET NUMBER: 7848-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 310/312-9900  
; TELEFAX: 310/478-8340  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 187 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-08-067-684-14

Query Match 13.8%; Score 87.5; DB 1; Length 187;  
Best Local Similarity 27.4%; Pred. No. 0.031;  
Matches 34; Conservative 15; Mismatches 56; Indels 19; Gaps 4;

Qy 3 VSOPPEIRTELGSAFLPCSFNASQGLAIGSVTWPRDEWVPKGVNRNGTPEFRGLAPL 62

Db 4 VAQPAVVLASSRGIAFVCEY-ASPGKATEVRVTVLQRADSQVTEVCAATYMGNELT-- 60

Qy 63 ASSRFLHD-----HQAEHLHVRVGRHDASIVYCRVEVL---GLGVGTNGTRLVVE 110

Db 61 -----FLDDSICTSGNQVNLTIQGLRANDTGLYICKVELMYPYPYLGNGTQIYVI 116

Qy 111 KEHP 114

Db 117 DPEP 120

## RESULT 15

US-08-008-898-14  
; Sequence 14, Application US/08008898  
; Patent No. 5770197  
; GENERAL INFORMATION:

; APPLICANT: Linsley, Peter S  
; APPLICANT: Ledbetter, Jeffrey A  
; APPLICANT: Damle, Nitin K  
; APPLICANT: Brady, William  
; TITLE OF INVENTION: CTLA4 RECEPTOR AND METHODS FOR ITS USE  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sheldon & Mak  
; STREET: 201 South Lake Avenue, Suite 800  
; CITY: Pasadena  
; STATE: California  
; COUNTRY: United States  
; ZIP: 91101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/008,898  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/723,617  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mandel, Saralynn  
; REGISTRATION NUMBER: 31,853  
; REFERENCE/DOCKET NUMBER: 7848  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (818) 796-4000  
; TELEFAX: (818) 795-6321  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 187 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-008-898-14

Query Match 13.8%; Score 87.5; DB 1; Length 187;  
Best Local Similarity 27.4%; Pred. No. 0.031;  
Matches 34; Conservative 15; Mismatches 56; Indels 19; Gaps 4;

Qy 3 VSOPPEIRTELGSAFLPCSFNASQGLAIGSVTWPRDEWVPKGVNRNGTPEFRGLAPL 62

Db 4 VAQPAVVLASSRGIAFVCEY-ASPGKATEVRVTVLQRADSQVTEVCAATYMGNELT-- 60

Qy 63 ASSRFLHD-----HQAEHLHVRVGRHDASIVYCRVEVL---GLGVGTNGTRLVVE 110

Db 61 -----FLDDSICTSGNQVNLTIQGLRANDTGLYICKVELMYPYPYLGNGTQIYVI 116

Qy 111 KEHP 114

Db 117 DPEP 120

Search completed: November 16, 2004, 19:17:43

Job time : 34.7401 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 16, 2004, 18:56:40 ; Search time 3.93103 Seconds  
(without alignments)  
465.048 Million cell updates/sec

Title: US-10-036-444-5  
Perfect score: 88  
Sequence: 1 VLLLRAGFYAVSLVAVG 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79: \*  
1: PIR1: \*  
2: PIR2: \*  
3: PIR3: \*  
4: PIR4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	53.4	835	2 T06590	probable beta-gala
2	46	52.3	724	2 T04340	beta-galactosidase
3	46	52.3	757	2 T03561	probable cellulose
4	44.5	50.6	479	2 T32293	aldenhyde dehydroge
5	44	50.0	184	2 C90157	hypothetical prote
6	43	48.9	466	2 AHI800	transmembrane effl
7	43	48.9	581	2 S03540	gene frizzled prot
8	42	47.7	217	2 F69512	conserved hypothet
9	42	47.7	271	2 B83918	hypothetical prote
10	42	47.7	388	2 B83228	probable MFS trans
11	42	47.7	466	2 AII426	transmembrane effl
12	42	47.7	560	2 S46096	probable membrane
13	42	47.7	658	2 S74246	sulfate transport
14	41	46.6	310	2 F71027	hypothetical prote
15	41	46.6	333	2 A70602	hypothetical prote
16	41	46.6	356	2 A70332	hypothetical prote
17	41	46.6	364	2 H83787	hypothetical prote
18	41	46.6	451	2 E90171	inorganic phosphat
19	40	45.5	498	2 T19901	hypothetical prote
20	40	45.5	135	2 E83466	conserved hypothet
21	40	45.5	154	2 F69477	NADH2 dehydrogenas
22	40	45.5	233	2 C95987	probable two-compo
23	40	45.5	245	2 I51323	proteolipid protei
24	40	45.5	288	2 T37709	hypothetical prote
25	40	45.5	303	2 T42703	hypothetical prote
26	40	45.5	328	2 C87673	4-hydroxybenzoate
27	40	45.5	342	2 AG3092	hypothetical prote
28	40	45.5	351	2 E64524	NADH2 dehydrogenas
29	40	45.5	351	2 G71983	hypothetical prote

30	40	45.5	382	2 H86930	probable secreted
31	40	45.5	401	2 F75037	hexuronate transpo
32	40	45.5	412	2 F97196	probable permease,
33	40	45.5	423	2 G71650	proline/betaine tr
34	40	45.5	424	2 H97870	proline/betaine tr
35	40	45.5	452	2 T45448	probable serine pr
36	40	45.5	507	2 E90540	hypothetical prote
37	40	45.5	514	2 S46733	hypothetical prote
38	40	45.5	572	2 T13740	probable hormone r
39	40	45.5	606	2 AC2425	ATP-binding protei
40	40	45.5	610	2 A85870	probable transport
41	40	45.5	610	2 H91025	probable transport
42	40	45.5	610	2 B65001	probable transport
43	40	45.5	1040	2 D81379	transmembrane effl
44	39.5	44.9	396	2 AD3012	conserved hypothet
45	39.5	44.9	492	2 C98272	hypothetical prote

#### ALIGNMENTS

##### RESULT 1

T06590  
probable beta-galactosidase (EC 3.2.1.23) - tomato  
C:Species: Lycopodium esculentum (tomato)  
C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
C:Accession: T06590  
R:Carey, A.T.; Holt, K.; Picard, S.; Wilde, R.; Tucker, G.A.; Bird, C.R.; Schuch, W.; S  
Plant Physiol. 108, 1099-1107, 1995  
A:Title: Tomato exo-(1-4)-beta-D-galactanase: isolation, changes during ripening in nor  
A:Reference number: 215780; MUID:95357407; PMID:7630937  
A:Accession: T06590  
A:Status: translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-835 <CAR>  
A:Cross-references: UNIPROT:P48980; EMBL:X83854; NID:G971484; PIDN:CAA58734.1; PID:G971  
A:Experimental source: cultivar Ailsa Craig; pericarp  
C:Superfamily: beta-galactosidase bga  
C:Keywords: glycosidase; hydrolase

Query Match 53.4%; Score 47; DB 2; Length 835;  
Best Local Similarity 62.5%; Pred. No. 8.6;  
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 LRAGFYAVSLVAVG 19  
||| :|||  
Db 527 LRAGNKISLLSIAVG 542

##### RESULT 2

T04340  
beta-galactosidase (EC 3.2.1.23) II precursor - tomato  
C:Species: Lycopodium esculentum (tomato)  
C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
C:Accession: T04340  
R:Smith, D.L.; Starrett, D.A.; Gross, K.C.  
Plant Physiol. 117, 417-423, 1998  
A:Title: A gene coding for tomato fruit beta-galactosidase II is expressed during fruit  
A:Reference number: 215296; MUID:98289087; PMID:9625694  
A:Accession: T04340  
A:Status: translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-724 <SMI>  
A:Cross-references: UNIPROT:O81100; EMBL:AF020390; NID:G3299895; PIDN:AAC25984.1; PID:G  
A:Experimental source: strain Rutgers; tissue-type tomato fruit  
C:Genetics:  
A:Gene: Bgal4  
C:Superfamily: beta-galactosidase bga  
C:Keywords: glycosidase; hydrolase  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:24-724/Product: beta-galactosidase II #status predicted <MAT>

Query Match 52.3%; Score 46; DB 2; Length 724;





C/Accession: S03540; S15708; S15709  
 R/Vinson, C.R.; Conover, S.; Adler, P.N.  
 Nature 338, 263-264, 1999  
 A/Title: A *Drosophila* tissue polarity locus encodes a protein containing seven potential  
 A/Reference number: S03540; MUID:89159415; PMID:2493583  
 A/Accession: S03540  
 A/Status: not compared with conceptual translation  
 A/Molecule type: mRNA  
 A/Residues: 1-581 <VIN>  
 A/Cross-references: UNIPROT:P18537  
 R/Adler, P.N.; Vinson, C.; Park, W.J.; Conover, S.; Klein, L.  
 Genetics 126, 401-416, 1990  
 A/Title: Molecular structure of a frizzled, a *Drosophila* tissue polarity gene.  
 A/Reference number: S15708; MUID:91060073; PMID:2174014  
 A/Accession: S15708  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-581 <ADL>  
 A/Cross-references: EMBL:X54648; NID:g7973; PIDN:CAA38460.1; PID:g804979  
 A/Accession: S15709  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-405, 'MY', 408, 'WOFHTIN' <AD2>  
 A/Cross-references: EMBL:X54648; NID:g7973; PIDN:CAA38461.1; PID:g804980  
 C/Genetics:  
 A/Gene: FlyBase: fz  
 A/Cross-references: FlyBase:FBgn0001085  
 A/Introns: 224/3; 264/3; 329/3; 405/1  
 C/Superfamily: fruit fly frizzled protein  
 C/Keywords: alternative splicing; transmembrane protein  
 F/1-26/Domain: signal sequence #status predicted <SIG>  
 F/27-581/Product: gene frizzled protein #status predicted <WAT>  
 Query Match 48.9%; Score 43; DB 2; Length 581;  
 Best Local Similarity 50.0%; Pred. No. 28;  
 Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
 QY 2 LLIRAGFYAVSFLSVAVG 19  
 DB 468 LMLRIGFFSGLFILPVG 485  
 RESULT 8  
 F69512  
 conserved hypothetical protein AF2102 - *Archaeoglobus fulgidus*  
 C/Species: *Archaeoglobus fulgidus*  
 C/Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
 C/Accession: F69512  
 R/Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson  
 Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.  
 Nature 390, 364-370, 1997  
 A/Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.  
 Smith, H.O.; Woese, C.R.; Venter, J.C.  
 A/Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo  
 A/Reference number: A69250; MUID:98049343; PMID:9389475  
 A/Accession: F69512  
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A/Molecule type: DNA  
 A/Residues: 1-217 <KLE>  
 A/Cross-references: UNIPROT:O28178; GB:AE000959; GB:AE000782; NID:g2689281; PIDN:AAB8914  
 Query Match 47.7%; Score 42; DB 2; Length 217;  
 Best Local Similarity 76.9%; Pred. No. 16;  
 Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 LLIRAGFYAVSFL 14  
 DB 198 LLLSAGLAVSFL 210  
 RESULT 9  
 B86918  
 C/Accession: S03540; S15708; S15709  
 R/Vinson, C.R.; Conover, S.; Adler, P.N.  
 Nature 338, 263-264, 1999  
 A/Title: A *Drosophila* tissue polarity locus encodes a protein containing seven potential  
 A/Reference number: S03540; MUID:89159415; PMID:2493583  
 A/Accession: S03540  
 A/Status: not compared with conceptual translation  
 A/Molecule type: mRNA  
 A/Residues: 1-581 <VIN>  
 A/Cross-references: UNIPROT:P18537  
 R/Adler, P.N.; Vinson, C.; Park, W.J.; Conover, S.; Klein, L.  
 Genetics 126, 401-416, 1990  
 A/Title: Molecular structure of a frizzled, a *Drosophila* tissue polarity gene.  
 A/Reference number: S15708; MUID:91060073; PMID:2174014  
 A/Accession: S15708  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-581 <ADL>  
 A/Cross-references: EMBL:X54648; NID:g7973; PIDN:CAA38460.1; PID:g804979  
 A/Accession: S15709  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-405, 'MY', 408, 'WOFHTIN' <AD2>  
 A/Cross-references: EMBL:X54648; NID:g7973; PIDN:CAA38461.1; PID:g804980  
 C/Genetics:  
 A/Gene: FlyBase: fz  
 A/Cross-references: FlyBase:FBgn0001085  
 A/Introns: 224/3; 264/3; 329/3; 405/1  
 C/Superfamily: fruit fly frizzled protein  
 C/Keywords: alternative splicing; transmembrane protein  
 F/1-26/Domain: signal sequence #status predicted <SIG>  
 F/27-581/Product: gene frizzled protein #status predicted <WAT>  
 Query Match 48.9%; Score 43; DB 2; Length 581;  
 Best Local Similarity 50.0%; Pred. No. 28;  
 Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
 QY 2 LLIRAGFYAVSFLSVAVG 19  
 DB 468 LMLRIGFFSGLFILPVG 485  
 RESULT 8  
 F69512  
 conserved hypothetical protein AF2102 - *Archaeoglobus fulgidus*  
 C/Species: *Archaeoglobus fulgidus*  
 C/Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
 C/Accession: F69512  
 R/Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson  
 Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.  
 Nature 390, 364-370, 1997  
 A/Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.  
 Smith, H.O.; Woese, C.R.; Venter, J.C.  
 A/Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo  
 A/Reference number: A69250; MUID:98049343; PMID:9389475  
 A/Accession: F69512  
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A/Molecule type: DNA  
 A/Residues: 1-217 <KLE>  
 A/Cross-references: UNIPROT:O28178; GB:AE000959; GB:AE000782; NID:g2689281; PIDN:AAB8914  
 Query Match 47.7%; Score 42; DB 2; Length 217;  
 Best Local Similarity 76.9%; Pred. No. 16;  
 Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 LLIRAGFYAVSFL 14  
 DB 198 LLLSAGLAVSFL 210  
 RESULT 9  
 B86918

hypothetical protein glpQ [imported] - *Mycobacterium leprae*  
 C/Species: *Mycobacterium leprae*  
 C/Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 09-Jul-2004  
 C/Accession: B86918  
 R/Cole, S.T.; Eigemeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; H.  
 R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd  
 eam, M.A.; Rutherford, K.M.  
 Nature 409, 1007-1011, 2001  
 A/Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; S.  
 A/Title: Massive gene decay in the leprosy bacillus.  
 A/Reference number: A86909; MUID:21128732; PMID:111234002  
 A/Accession: B86918  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-271 <STO>  
 A/Cross-references: UNIPROT:Q9CDC5; GB:AL450380; NID:gl3092456; PIDN:CAC29582.1; GSPDB:  
 C/Genetics:  
 A/Gene: glpQ  
 Query Match 47.7%; Score 42; DB 2; Length 271;  
 Best Local Similarity 57.9%; Pred. No. 20;  
 Matches 11; Conservative 1; Mismatches 7; Indels 0; Gaps 0;  
 QY 1 VLLIRAGFYAVSFLSVAVG 19  
 DB 184 VLLGRAGRYLTSAATAVG 202  
 RESULT 10  
 B83228  
 Probable MFS transporter PA3336 [imported] - *Pseudomonas aeruginosa* (strain PA01)  
 C/Species: *Pseudomonas aeruginosa*  
 C/Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
 C/Accession: B83228  
 R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B.  
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Latbig, K.; Lim.  
 ; Lory, S.; Olson, M.V.  
 Nature 406, 959-964, 2000  
 A/Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic path  
 A/Reference number: A82950; MUID:20437337; PMID:10984043  
 A/Accession: B83228  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-388 <STO>  
 A/Cross-references: UNIPROT:Q9HYQ9; GB:AE004756; GB:AE004966; PIDN:AAG067.  
 A/Experimental source: strain PA01  
 C/Genetics:  
 A/Gene: PA3336  
 C/Superfamily: Streptomyces lividans chloramphenicol resistance protein  
 Query Match 47.7%; Score 42; DB 2; Length 388;  
 Best Local Similarity 53.3%; Pred. No. 28;  
 Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
 QY 5 RAGFYAVSFLSVAVG 19  
 DB 157 RASFFAVALVAVLG 171  
 RESULT 11  
 A11426  
 transmembrane efflux protein homolog lmo2818 [imported] - *Listeria monocytogenes* (strai  
 C/Species: *Listeria monocytogenes*  
 C/Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 09-Jul-2004  
 C/Accession: A11426  
 R/Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker,  
 ; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi H  
 D.; Jones, L.M.; Karst, U.  
 Science 294, 849-852, 2001  
 A/Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurapat, G.; Madueno, E.; Maitournam, A.; M.  
 ck, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland  
 A/Title: Comparative Genomics of *Listeria* species.  
 A/Reference number: AB1077; MUID:21537279; PMID:11679669

A;Accession: A11426  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-456 <GLA>  
A;Cross-references: UNIPROT  
A;Experimental source:   
C;Genetics:  
C;Gene: lmo2818 -  
C;Superfamily: multidrug

Query Match 47.7%; Score 42; DB 2; Length 466;  
Best Local Similarity 52.9%; Pred. No. 33;  
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

RESULT 12  
S46096  
probable membrane protein YBR220c - yeast (*Saccharomyces cerevisiae*)  
N;Alternate names: hypothetical protein YBR1510  
C;Species: *Saccharomyces cerevisiae*  
C;Date: 26-Aug-1994 #sequence\_revision 09-Sep-1994 #text\_change 09-Jul-2004  
C;Accession: S46096  
R;Dubois, E.; El Bakoury, M.; Glansdorff, N.; Messenguy, F.; Pierard, A.; Scherens, B.;  
submitted to the Protein Sequence Database, August 1994  
A;Reference number: S45782  
A;Accession: S46096  
A;Molecule type: DNA  
A;Residues: 1-560 <DUE>  
A;Cross-references: UNIPROT:P39318; EMBL:Z36088; NID:g536609; PID:g536611; GSFPB:GN000002  
A;Experimental source: strain S288C  
C;Genetics:

```
Query Match      47.7%; Score 42; DB 2; Length 560;
Best Local Similarity 36.8%; Pred. No. 40;
Matches 7; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
```

RESULT 13  
S74246  
sulfate transport protein - Arabidopsis thaliana  
N;Alternate names: sulfate transporter  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 28-Oct-1996 #sequence\_revision 14-Nov-1997 #text\_change 09-Jul-2004  
C;Accession: S74246  
P;Rakahashi, H.; Sasaki, N.; Noji, M.; Saito, K.  
FEBS Lett. 392, 35-39, 1996  
A;Title: Isolation and characterization of a cDNA encoding a sulfate transporter from *Arabidopsis thaliana*.  
A;Reference number: S74246; MUID:96368029; PMID:8772182  
A;Accession: S74246  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA

A:Residues: 1-658 <TAX>  
 C:Cross-references: UNIPROT:P92946; EMBL:D85416; NID:gl498119; PID:gl498120  
 C:Superfamily: sulfate transport protein  
 C:Keywords: sulfate transport; transmembrane protein  
 F:99-109/Domain: transmembrane #status predicted <TM1>  
 F:119-134/Domain: transmembrane #status predicted <TM2>  
 F:140-156/Domain: transmembrane #status predicted <TM3>  
 F:172-190/Domain: transmembrane #status predicted <TM4>  
 F:194-217/Domain: transmembrane #status predicted <TM5>  
 F:233-271/Domain: transmembrane #status predicted <TM6>  
 F:278-299/Domain: transmembrane #status predicted <TM7>  
 F:338-353/Domain: transmembrane #status predicted <TM8>  
 F:371-388/Domain: transmembrane #status predicted <TM9>  
 F:408-430/Domain: transmembrane #status predicted <TM10>  
 F:435-457/Domain: transmembrane #status predicted <TM11>  
 F:454-489/Domain: transmembrane #status predicted <TM12>

Query Match	47.7%	Score 42;	DB 2;	Length 658;
Best Local Similarity	50.0%	Pred. No. 46;		
Matches	9;	Conservative	3;	Mismatches 6;
				Indels 0;
				Gaps 0;

RESULT 14

F71027  
hypothetical protein PH1514 - Pyrococcus horikoshii  
C:Species: Pyrococcus horikoshii  
C:Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 09-Jul-2004  
C:Accession: F71027  
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin  
M.; Ohtuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi  
DNA Res. 5, 55-76, 1998  
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a  
A:Reference Number: A71000, MUID:98344137; PMID:9679194  
A:Accession: F71027  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-310 <RAW>  
A:Cross-References: UNIPROT:O59183; GB:AP000006; NID:G3236133; PIDN:BAA30622.1; PID:G325  
A:Experimental source: strain OT3  
A:Note: this accession replaces an interim accession for a sequence replaced by GenBank  
C:Genetics:  
A:Gene: PH1514

```
Query Match      46.6%; Score 41; DB 2; Length 310;
Best Local Similarity 58.3%; Pred. No. 33;
Matches 7: Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

RESULT 15

A70602      hypothetical protein RV0998 - Mycobacterium tuberculosis (strain H37RV)  
C:Species: Mycobacterium tuberculosis  
C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004  
C:Accession: A70602  
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, E.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, Nature 393, 537-544, 1998  
A:Authors: Soares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.  
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the genome  
A:Reference number: A70500; MIMD:98295987; PMID:9634230  
A:Accession: A70602  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-333 <COL>

A:Accession: A70002  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-333 <COL>

A:Cross-references: UNIPROT:O05581; GB:Z94752; GB:AL123456; NID:G3261731; PIDN:CAB08156.  
A:Experimental source: strain H37Rv  
C:Genetics:  
A:Gene: RV0998

Query Match 46.6%; Score 41; DB 2; Length 333;  
Best Local Similarity 55.6%; Pred. No. 35;  
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Cy 2 LLRAGFYAVSFLSVAVG 19  
:|||||:|:|:  
Db 46 VLLRQGEPAVSFLLISSG 63

Search completed: November 16, 2004, 19:15:54  
Job time : 6.93103 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model  
Run on: November 16, 2004, 18:56:15 ; Search time 21.2175 Seconds  
(without alignments)  
515.240 Million cell updates/sec

Title: US-10-036-444-5  
Perfect score: 88  
Sequence: 1 VLLLRAGFYAVSFLSVAVG 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_02:\*

- 1: uniprot\_sprot:\*
- 2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	88	100.0	176	1 NCT3_MACFA	P61483 macaca fasc
2	88	100.0	201	1 NCT3_HUMAN	Q14931 homo sapien
3	88	100.0	201	1 NCT3_PANTR	P61484 pan troglod
4	85	96.6	180	1 NCT3_MACMU	Q8m102 macaca mula
5	70	79.5	192	1 NCT3_RAT	Q8cfd9 rattus norv
6	51	58.0	847	2 Q9SCW1	Q9scw1 arabidopsis
7	51	58.0	847	2 Q8RXC1	Q8rxc1 arabidopsis
8	49	55.7	610	2 Q7VEF7	Q7vef7 prochloroco
9	48	54.5	707	2 Q6S761	Q6s761 cicor ariet
10	48	54.5	721	2 Q9ZFP0	Q9zfp0 carica papa
11	47	53.4	571	2 Q6BUP5	Q6bup5 debaryomyce
12	47	53.4	835	1 EGAL_LYCES	P48980 lycopersico
13	47	53.4	835	2 CAA10174	Caa10174 lycopersi
14	47	53.4	835	2 AAF21626	Aaf21626 lycopersi
15	47	53.4	838	2 Q9ZF11	Q9zf11 lycopersico
16	46	52.3	724	2 Q81100	Q81100 lycopersico
17	46	52.3	724	2 Q9TOP6	Q9top6 lycopersico
18	46	52.3	757	2 Q80899	Q80899 arabidopsis
19	46	52.3	3763	2 Q8T2A1	Q8t2a1 dictyostel
20	45	51.1	230	2 Q7X9C6	Q7x9c6 pyrus pyrif
21	45	51.1	270	2 Q8RD77	Q8rd77 thermoanaer
22	45	51.1	376	2 Q3FVH5	Q3fvh5 prunus arme
23	45	51.1	843	2 Q93X58	Q93x58 fragaria an
24	45	51.1	1561	2 Q888F2	Q888f2 pseudomonas
25	44.5	50.6	479	2 Q86001	Q86001 sphingomona
26	44	50.0	146	2 Q70121	Q70121 oncorhynch
27	44	50.0	146	2 CAE45583	CaE45583 oncorhync
28	44	50.0	184	2 Q880V8	Q880v8 sulfobab
29	44	50.0	351	2 Q8G3L8	Q8g3l8 bifidobacte
30	44	50.0	381	2 Q46A_DROME	Q46a_drosophila
31	44	50.0	476	2 Q82WR1	Q82wr1 nitrosomona

32	44	50.0	591	2 Q79YS2	Q79ys2 streptococc
33	44	50.0	591	2 Q8K8X7	Q8k8x7 streptococc
34	44	50.0	591	2 Q8P300	Q8p300 streptococc
35	44	50.0	602	2 Q8CR29	Q8cr29 staphylococ
36	44	50.0	739	2 Q9M5J3	Q9m5j3 phaseolus a
37	44	50.0	826	2 Q6EM02	Q6em02 sandersonia
38	44	50.0	845	2 Q9LLS9	Q9lls9 lycopersico
39	43.5	49.4	202	2 Q8BWB7	Q8bwb7 mus musculu
40	43.5	49.4	306	2 Q8BX24	Q8bx24 mus musculu
41	43.5	49.4	334	2 Q8BKX2	Q8bkx2 mus musculu
42	43.5	49.4	355	1 S3SD_HUMAN	Q9rtn3 homo sapien
43	43	48.9	85	2 Q6BI02	Q6bi02 debaryomyce
44	43	48.9	160	2 Q8M0F0	Q8m0f0 cryptococcu
45	43	48.9	202	2 Q85T00	Q85t00 cryptococcu

ALIGNMENTS

RESULT 1  
NCT3\_MACFA  
ID NCT3\_MACFA STANDARD; PRT; 176 AA.  
AC P61483; Q95JB8;  
DT 05-JUL-2004 (Rel. 44, Created)  
DT 05-JUL-2004 (Rel. 44, Last sequence update)  
DE Natural cytotoxicity triggering receptor 3 precursor (Natural killer cell p30-related protein) (NKp30) (NK-p30).  
GN Name=NCR3;  
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae; Cercopithecinae; Macaca.  
OX NCBI\_TaxID=9541;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lymphoid;  
RA Rizzi M., Biassoni R.;  
RT "Non MFC specific natural cytotoxicity receptors (NCR) expressed in Macaca fascicularis lymphoid cells."  
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Cytotoxicity activating receptor that may contribute to the increased efficiency of activated natural killer (NK) cells to mediate tumor cell lysis (by similarity).  
CC -!- SUBUNIT: Interacts with CD32 (By similarity).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
CC -!- SIMILARITY: Belongs to natural cytotoxicity receptor (NCR) family.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
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CC EMBL; AJ279389; CAC41081.1; -.  
CC HSP; P16410; I185.  
CC InterPro; IPR003599; IG.  
CC InterPro; IPR007110; IG-like.  
CC Pfam; PF00047; IG; 1.  
CC SMART; SM00409; IG; 1.  
CC PROSITE; PS50835; IG\_LIKE; 1.  
CC Glycoprotein; Immunoglobulin domain; Receptor; Signal; Transmembrane. Potential.  
FT SIGNAL 1 18  
FT CHAIN 19 176  
FT Natural cytotoxicity triggering receptor 3.  
FT DOMAIN 19 135  
FT Extracellular (Potential).  
FT TRANSMEM 136 156  
FT Potential.  
FT DOMAIN 157 176  
FT Cytoplasmic (Potential).  
FT DOMAIN 19 126  
FT IG-like.  
FT DISULFID 39 108  
FT By similarity.

FT CARBOHYD 42 42 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 121 121 N-linked (GlcNAc...) (Potential).  
 SQ SEQUENCE 176 AA; 19251 MW; 97B2A3B625E4AD54 CRC64;

Query Match 100.0%; Score 88; DB 1; Length 176;  
 Best Local Similarity 100.0%; Pred. No. 2,7e+06;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLLLRAGFYAVSFSLVAVG 19  
 Db 139 VLLLRAGFYAVSFSLVAVG 157

RESULT 2

NCT3\_HUMAN STANDARD; PRT; 201 AA.  
 ID NCT3\_HUMAN O14930; O14932; O95667; O95668; O95669;  
 AC O14933; O14930; O14932; O95667; O95668; O95669;  
 DT 05-JUL-2004 (Rel. 44, Created)  
 DT 05-JUL-2004 (Rel. 44, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Natural cytotoxicity triggering receptor 3 precursor (Natural killer  
 DE cell p30-related protein) (Nkp30) (NK-P30).  
 GN Name=NCR3; Synonyms=IC7;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBT\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 2), TISSUE SPECIFICITY, INTERACTION WITH  
 RP CD32, AND FUNCTION.  
 RC TISSUE=Lymphoid;  
 RX PubMed=10562324;  
 RA Pende D., Parolini S., Pessino A., Sivori S., Augugliaro R.,  
 RA Morelli L., Marsenaro E., Accame L., Malaipina A., Biassoni R.,  
 RA Bottino C., Moretta L., Moretta A.;  
 RT "Identification and molecular characterization of Nkp30, a novel  
 RT triggering receptor involved in natural cytotoxicity mediated by human  
 RT natural killer cells.";  
 RL J. Exp. Med. 190:1505-1516(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 2), TISSUE SPECIFICITY, AND INTERACTION  
 RP WITH CD32.  
 RC TISSUE=Peripheral blood;  
 RA Sato M., Yabe T., Ohashi J., Tsuchiya N., Hanaoka K., Tokunaga K.,  
 RA Fuji T.;  
 RT "Identification of two novel single nucleotide polymorphisms in the  
 RT Nkp30 gene in human natural killer cells.";  
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4; 5 AND 6).  
 RX MEDLINE=99218514; PubMed=10202016;  
 RA Neville M.J., Campbell R.D.;  
 RT "A new member of the Ig superfamily and a V-ATPase G subunit are among  
 RT the predicted products of novel genes close to the TNF locus in the  
 RT human MHC.";  
 RL J. Immunol. 162:4745-4754(1999).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
 RC TISSUE=Spleen;  
 RX MEDLINE=9642187; PubMed=8824804;  
 RA Nalabolu S.R., Shukla H., Nallur G., Parimoo S., Weissman S.M.;  
 RT "Genes in a 220-kb region spanning the TNF cluster in human MHC.";  
 RL Genomics 31:215-222(1996).  
 RN [5]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RX PubMed=1465967; DOI=10.1101/gr.1736803;  
 RA Xie T., Rowen L., Aguado B., Ahearn M.E., Madan A., Qin S.,  
 RA Campbell R.D., Hood L.;  
 RT "Analysis of the gene-dense major histocompatibility complex class III  
 RT region and its comparison to mouse.";  
 RL Genome Res. 13:2621-2636(2003).  
 RN [6]  
 RP SEQUENCE FROM N.A. (ISOFORM 3).

RA Shiina S., Tamiya G., Oka A., Inoko H.;  
 RT "Homo sapiens 2,929,817bp genomic DNA of 6p21.3 HLA class I region.";  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Blood;  
 RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.B., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan K., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udwin T.B., Toshyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -!- FUNCTION: Cytotoxicity activating receptor that may contribute to  
 CC the increased efficiency of activated natural killer (NK) cells to  
 CC mediate tumor cell lysis.  
 CC -!- SUBUNIT: Interacts with CD32.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=6;  
 CC Name=1; Synonyms=IC7a;  
 CC IsoId=O14931-1; Sequence=Displayed;  
 CC Note=No experimental confirmation available;  
 CC Name=2; Synonyms=IC7c;  
 CC IsoId=O14931-2; Sequence=VSP\_010413;  
 CC Note=No experimental confirmation available;  
 CC Name=3; Synonyms=IC7b;  
 CC IsoId=O14931-3; Sequence=VSP\_010412;  
 CC Note=No experimental confirmation available;  
 CC Name=4; Synonyms=IC7e;  
 CC IsoId=O14931-4; Sequence=VSP\_010411;  
 CC Note=No experimental confirmation available;  
 CC Name=5; Synonyms=IC7f;  
 CC IsoId=O14931-5; Sequence=VSP\_010411, VSP\_010413;  
 CC Note=No experimental confirmation available;  
 CC Name=6; Synonyms=IC7d;  
 CC IsoId=O14931-6; Sequence=VSP\_010411, VSP\_010412;  
 CC Note=No experimental confirmation available;  
 CC -!- TISSUE SPECIFICITY: Selectively expressed by all resting and  
 CC activated NK cells and weakly expressed in spleen.  
 CC -!- SIMILARITY: Belongs to natural cytotoxicity receptor (NCR) family.  
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.

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EMBL; AJ223153; CAB54004.1; -  
 EMBL; AB055881; BAB78472.1; -  
 EMBL; Y14768; CAA75063.1; -  
 EMBL; Y14768; CAA75064.1; -  
 EMBL; Y14768; CAA75065.1; -  
 EMBL; Y14768; CAA75066.1; -  
 EMBL; Y14768; CAA75067.1; -  
 EMBL; Y14768; CAA75068.1; -







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RL Genome Res. 14:631-639(2004).
CC -!- FUNCTION: Cytotoxicity activating receptor that may contribute to
CC the increased efficiency of activated natural killer (NK) cells to
CC mediate tumor cell lysis (CD3Z (By similarity)).
CC -!- SUBUNIT: Interacts with CD3Z (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -!- SIMILARITY: Belongs to natural cytotoxicity receptor (NCR) family.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC -----
DR EMBL; AJ430418; CAD23066.1; -.
DR EMBL; AJ430419; CAD23067.2; -.
DR EMBL; AJ430420; CAD23067.2; JOINED.
DR EMBL; AY273824; AAL13457.1; -.
DR EMBL; EX883046; CAB84000.1; -.
DR HSP; P03793; IDOT.
DR RGD; 727881; 1C7.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; Ig; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Glycoprotein; Immunoglobulin domain; Polymorphism; Receptor; Signal;
KW Transmembrane.
FT SIGNAL 1 18 Potential.
FT CHAIN 19 192 Natural cytotoxicity triggering receptor
FT DOMAIN 19 147 Extracellular (Potential).
FT TRANSMEM 148 168 Potential.
FT DOMAIN 169 192 Cytoplasmic (Potential).
FT DOMAIN 19 126 IG-like.
FT DISULFID 39 108 By similarity.
FT VARIANT 7 7 I -> V.
FT VARIANT 19 19 I -> V.
FT VARIANT 82 82 A -> V.
FT VARIANT 138 138 A -> T.
FT CONFLICT 135 135 A -> V (in Ref. 2).
SQ SEQUENCE 192 AA; 20470 MW; 7FC84FB25D2D2377 CRC64;

Query Match 79.5%; Score 70; DB 1; Length 192;
Best Local Similarity 83.3%; Pred. No. 0.0027;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LLLRAGFYAVSFLSVATG 19
Db 148 LLLRAGVYALSVATG 165

RESULT 6
Q9SCW1 PRELIMINARY; PRT; 847 AA.
AC Q9SCW1
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Beta-galactosidase (EC 3.2.1.23).
GN Name=EGAL1;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsiis.
OX NCBI_TaxID=3702;
RN [1]
RN SEQUENCE FROM N.A.
RA Gy I., Kreis M., Lecharny A.;
RA Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.

Query Match 79.5%; Score 70; DB 1; Length 192;
Best Local Similarity 83.3%; Pred. No. 0.0027;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LLLRAGFYAVSFLSVATG 19
Db 148 LLLRAGVYALSVATG 165

RESULT 6
Q9SCW1 PRELIMINARY; PRT; 847 AA.
AC Q9SCW1
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Beta-galactosidase (EC 3.2.1.23).
GN Name=EGAL1;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsiis.
OX NCBI_TaxID=3702;
RN [1]
RN SEQUENCE FROM N.A.
RA Gy I., Kreis M., Lecharny A.;
RA Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
```

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RN SEQUENCE FROM N.A.
RP MEDLINE=20363099; PubMed=10907853;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT Sequence features of the regions of 4,251,695 bp covered by ninety P1,
RT TAC and BAC clones.";
RL DNA Res. 7:217-221(2000).
RN [3]
RN SEQUENCE FROM N.A.
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing beta-D-
CC galactose residues in beta-D-galactosides.
CC -!- SIMILARITY: Belongs to family 35 of glycosyl hydrolases.
DR EMBL; AJ270297; CAB64737.1; -.
DR EMBL; AP001307; BAB01923.1; -.
DR GO; GO:0009341; C:beta-galactosidase complex; IEA.
DR GO; GO:0004565; F:beta-galactosidase activity; IEA.
DR GO; GO:0004578; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR008979; Gal bind like.
DR InterPro; IPR009222; Gal lectin.
DR InterPro; IPR001944; Glyco_hydro_35.
DR InterPro; IPR002016; Peroxidase.
DR Pfam; PF02140; Gal_lectin; 1.
DR Pfam; PF01301; Glyco_hydro_35; 1.
DR PRINTS; PR00742; GLHYDRLASE35.
DR PRODOM; PD005612; Gal lectin; 1.
DR PROSITE; PS01182; GLYCOSYL_HYDROL_F35; 1.
DR PROSITE; PS00435; PEROXIDASE_1; UNKNOWN_1.
DR PROSITE; PS50228; SUEL_LECTIN; 1.
KW Glycosidase; Hydrolase; Signal.
FT SIGNAL 1 32
FT CHAIN 33 847 putative beta-galactosidase.
SQ SEQUENCE 847 AA; 93658 MW; 91C13DE26A4CF4AD CRC64;

Query Match 58.0%; Score 51; DB 2; Length 847;
Best Local Similarity 62.5%; Pred. No. 13;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 LRAGFYAVSFLSVATG 19
Db 539 LRAGFNKAILSATG 554

RESULT 7
Q9RWC1 PRELIMINARY; PRT; 847 AA.
ID Q9RWC1
AC Q9RWC1
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Galactosidase, putative.
GN Name=At3g13750;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsiis.
OX NCBI_TaxID=3702;
RN [1]
RN SEQUENCE FROM N.A.
RA Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk K., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RA Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing beta-D-
CC galactose residues in beta-D-galactosides.
CC -!- SIMILARITY: Belongs to family 35 of glycosyl hydrolases.
```

DR EMBL; AY093197; AAM13196.1; -  
 DR GO; GO:0009341; C:beta-galactosidase complex; IEA.  
 DR GO; GO:0004565; F:beta-galactosidase activity; IEA.  
 DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.  
 DR GO; GO:0005529; F:sugar binding; IEA.  
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
 DR InterPro; IPR008979; Gal\_bind\_like.  
 DR InterPro; IPR000922; Gal\_lectin.  
 DR InterPro; IPR001944; Glyco\_hydro\_35.  
 DR InterPro; IPR002016; Peroxidase.  
 DR Pfam; PF02140; Gal\_lectin; 1.  
 DR Pfam; PF01301; Glyco\_hydro\_35; 1.  
 DR PRINTS; PR00742; GLHYDRLASE35.  
 DR PROSITE; PS005612; Gal\_lectin; 1.  
 DR PROSITE; PS01182; GLYCOSYL\_HYDROL\_F35; 1.  
 DR PROSITE; PS00435; PEROXIDASE\_1; UNKNOWN\_1.  
 DR PROSITE; PS0228; SUEL\_LECTIN; 1.  
 KW Glycosidase; Hydrolase.  
 SQ SEQUENCE 847 AA; 93672 MW; 0F9E12685426C5DA CRC64;  
 Query Match 58.0%; Score 51; DB 2; Length 847;  
 Best Local Similarity 62.5%; Pred.No. 13;  
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 QY 4 LRAGFYAVSFLSVAVG 19  
 Db 539 LRAGFNKIALSLAVG 554  
 RESULT 8  
 Q7VEF7 PRELIMINARY; PRT; 610 AA.  
 AC Q7VEF7;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE ABC-type multidrug transport system ATPase and permease components; OrderedLocusNames=Pro00056;  
 GN Name=ndb; OrderedLocusNames=Pro00056;  
 OS Prochlorococcus marinus.  
 OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;  
 OC Prochlorococcus.  
 OX NCBI\_TaxID=1219;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SARG / CCMP 1375 / SS120;  
 RX MEDLINE=22810154; PubMed=12917486;  
 RA Dufresne A., Salanoubat M., Partensky F., Artiguenave F., Axmann I.M., Barbe V., Duprat S., Galperin M.Y., Koonin E.V., Le Gall F., Makarova K.S., Ostrowski M., Oztas S., Robert C., Rogozin I.B., Scanlan D.J., Tandeau de Marsac N., Weissenbach J., Wincker P., Wolf Y.I., Hess W.R.;  
 RA "Genome sequence of the cyanobacterium Prochlorococcus marinus SS120, a nearly minimal oxypotrophic genome."  
 RL Proc. Natl. Acad. Sci. U.S.A. 100:10020-10025 (2003).  
 CC -!- SIMILARITY: Belongs to the ABC transporter family.  
 DR EMBL; AE017161; AAP99102.1; -  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005524; P:ATP binding; IEA.  
 DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti...; IEA.  
 DR GO; GO:0006166; F:nucleotide binding; IEA.  
 DR GO; GO:0006101; P:transport; IEA.  
 DR InterPro; IPR003593; AAA\_ATPase.  
 DR InterPro; IPR011527; ABC\_membrane\_1.  
 DR InterPro; IPR001140; ABC\_TM\_transp.  
 DR InterPro; IPR003439; ABC\_transporter.  
 DR Pfam; PF00664; ABC\_membrane; 1.  
 DR Pfam; PF00005; ABC\_tran; 1.  
 DR ProDom; PD000006; ABC\_transporter; 1.  
 DR SMART; SM00382; AAA; 1.  
 DR PROSITE; PS50929; ABC\_TM1F; 1.  
 DR PROSITE; PS00211; ABC\_TRANSPORTER\_1; 1.  
 DR PROSITE; PS50893; ABC\_TRANSPORTER\_2; 1.

KW ATP-binding; Complete proteome.  
 SQ SEQUENCE 610 AA; 68701 MW; EBF39690C516DCDA CRC64;  
 Query Match 55.7%; Score 49; DB 2; Length 610;  
 Best Local Similarity 44.4%; Pred.No. 21;  
 Matches 8; Conservative 7; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 VLLLRAGFYAVSFLSVAVG 18  
 Db 156 ILQVSGFFIVSFISAI 173  
 RESULT 9  
 O65761 PRELIMINARY; PRT; 707 AA.  
 AC O65761;  
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Beta-galactosidase (EC 3.2.1.23) (Fragment).  
 OS Cicer arietinum (Chickpea) (Garbanzo).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eucosids I; Fabales; Fabaceae; Papilionoideae; Cicereae; Cicer.  
 OX NCBI\_TaxID=3827;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Etisolated epicotyl;  
 RA Dopico B., Batehan R., Labrador E.;  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 CC -!- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing beta-D-galactose residues in beta-D-galactosides.  
 CC -!- SIMILARITY: Belongs to family 35 of glycosyl hydrolases.  
 DR EMBL; AJ006771; CA07236.1; -  
 DR GO; GO:0009341; C:beta-galactosidase complex; IEA.  
 DR GO; GO:0004565; F:beta-galactosidase activity; IEA.  
 DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.  
 DR GO; GO:0005529; F:sugar binding; IEA.  
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
 DR InterPro; IPR008979; Gal\_bind\_like.  
 DR InterPro; IPR000922; Gal\_lectin.  
 DR InterPro; IPR001944; Glyco\_hydro\_35.  
 DR Pfam; PF02140; Gal\_lectin; 1.  
 DR Pfam; PF01301; Glyco\_hydro\_35; 1.  
 DR PRINTS; PR00742; GLHYDRLASE35.  
 DR ProDom; PD005612; Gal\_lectin; 1.  
 DR PROSITE; PS01182; GLYCOSYL\_HYDROL\_F35; 1.  
 DR PROSITE; PS0228; SUEL\_LECTIN; 1.  
 KW Glycosidase; Hydrolase.  
 FT NON TER 1  
 SQ SEQUENCE 707 AA; 77903 MW; 85C970DDA8A92A31 CRC64;  
 Query Match 54.5%; Score 48; DB 2; Length 707;  
 Best Local Similarity 68.8%; Pred.No. 35;  
 Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 QY 4 LRAGFYAVSFLSVAVG 19  
 Db 399 LRAGWNKISLSVAVG 414  
 RESULT 10  
 Q9ZP30 PRELIMINARY; PRT; 721 AA.  
 AC Q9ZP30;  
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Beta-galactosidase precursor (EC 3.2.1.23).  
 OS Carica papaya (Papaya).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eucosids II; Brassicales; Caricaceae; Carica.

```

OX NCBI_TaxID=3649;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Mesocarp;
RA Othman R., Chco T.S., Ali Z.M., Zainal Z., Lazan H.;
RT "A full-length beta-galactosidase cDNA sequence from ripening
RL papaya.";
CC -1- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing beta-D-
CC galactose residues in beta-D-galactosides.
CC -1- SIMILARITY: Belongs to family 35 of glycosyl hydrolases.
DR EMBL; AF064786; AAC7377.1; -.
DR GO; GO:0009341; C:beta-galactosidase complex; IEA.
DR GO; GO:0004565; F:beta-galactosidase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR008979; Gal bind like.
DR InterPro; IPR001944; Glyco_hydro_35.
DR Pfam; PF01301; Glyco_hydro_35; 1.
DR PRINTS; PR00742; GLHYDRLASE35.
DR PROSITE; PS01182; GLYCOSYL_HYDROL_F35; 1.
DR Glycosidase; Hydrolase; Signal.
FT SIGNAL 1 18 Potential.
FT CHAIN 19 721 beta galactosidase.
SQ SEQUENCE 721 AA; 80985 MW; 841BF5E16C399617 CRC64;

Query Match 54.5%; Score 48; DB 2; Length 721;
Best Local Similarity 68.8%; Pred. No. 36;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 LRAGFYAVSFSLVAVG 19
Db 526 LRAGVNKSLLSIAVG 541

RESULT 11
O6BUP5 PRELIMINARY; PRT; 571 AA.
AC Q8BUP5
DT 01-OCT-2004 (TrEMBLrel. 28, Created)
DT 01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Similar to sp|P38318 Saccharomyces cerevisiae YBR220c.
GN ORFNames=DEHACG100439;
OC Debaryomyces hansenii (Yeast) (Torulaspora hansenii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Debaryomyces.
OX NCBI_TaxID=4959;
RP SEQUENCE FROM N.A.
RC GENOLEVURES;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Tallia E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boistrave A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jaumiaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.M., Nikolski M., Ozias S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Svennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zenou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J.,
RA Winkler P., Souciet J.L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS767;
RA Genoscode;
RA Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.

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DR EMBL; CR382135; CAG86145.1; -.
SQ SEQUENCE 571 AA; 63970 MW; 02E730425004ABBD CRC64;

Query Match 53.4%; Score 47; DB 2; Length 571;
Best Local Similarity 47.4%; Pred. No. 43;
Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 VLLLRAGFYAVSFSLVAVG 19
Db 525 VLLLRDGFYINFFCIVCG 543

RESULT 12
BGAL LYCES
ID BGAL LYCES STANDARD; PRT; 835 AA.
AC P48980;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Beta-galactosidase precursor (EC 3.2.1.23) (Lactase) (Acid beta-
DE galactosidase) (Exo-(1-->4)-beta-D-galactanase).
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.; AND PARTIAL SEQUENCE.
RC STRAIN=cv. Ailsa Craig; TISSUE=Pericarp;
RX MEDLINE=95357407; PubMed=7630937;
RA Carey A.T., Holt K., Picard S., Wilde R., Tucker G.A., Bird C.R.,
RA Schuch W., Seymour G.B.;
RT "Tomato exo-(1-->4)-beta-D-galactanase. Isolation, changes during
RT ripening in normal and mutant tomato fruit, and characterization of a
RT related cDNA clone.";
RL Plant Physiol. 108:1099-1107(1995).
CC -1- FUNCTION: Involved in cell wall degradation. Degrades
CC polysaccharides containing beta-(1-->4)-linked galactans, acting
CC as an exo-(1-->4)-beta-D-galactanase.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing beta-D-
CC galactose residues in beta-D-galactosides.
CC -1- MISCELLANEOUS: Has a pH optimum of 4.5.
CC -1- SIMILARITY: Belongs to family 35 of glycosyl hydrolases.
CC -1- SIMILARITY: Contains 1 SUEL-type lectin domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X83854; CAA58734.1; -.
DR PIR; T06590; T06590.
DR InterPro; IPR008979; Gal_bind_like.
DR InterPro; IPR000922; Gal_lectin.
DR InterPro; IPR001944; Glyco_hydro_35.
DR Pfam; PF01301; Glyco_hydro_35; 1.
DR Pfam; PF01301; Glyco_hydro_35; 1.
DR PRINTS; PR00742; GLHYDRLASE35.
DR PRODOM; PD005612; Gal_lectin; 1.
DR PROSITE; PS01182; GLYCOSYL_HYDROL_F35; 1.
DR PROSITE; PS0228; SUEL.LECTIN; 1_22.
KW Direct protein sequencing; Glycosidase; Hydrolase; Signal.
FT SIGNAL 1 22
FT CHAIN 23 835 Beta-galactosidase.
FT DOMAIN 749 835 SUEL-type lectin.
FT ACT_SITE 180 180 Proton donor (Potential).
FT ACT_SITE 249 249 Nucleophile (Potential).
SQ SEQUENCE 835 AA; 93336 MW; 94C9685F95C4A646 CRC64;

Query Match 53.4%; Score 47; DB 1; Length 835;

```

Best Local Similarity 62.5%; Pred. No. 60;  
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 LRAGFYAVSFLSVAVG 19  
DB 527 LRAGVKNISLLSIAGV 542

RESULT 13  
CAA10174 PRELIMINARY; PRT; 835 AA.  
AC CAA10174;  
DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
DE SS-galactosidase precursor (EC 3.2.1.23).  
GN TEG1B.  
OS Lycopersicon esculentum (Tomato).  
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;  
OC Solanales; Solanaceae; Solanum.  
OX NCBI\_TaxID=4081;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV. Money maker;  
RA De Silva J., 22  
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ012797; CAA10174.1; -  
FT SIGNAL 1 22 POTENTIAL.  
FT CHAIN 23 835 SS-GALACTOSIDASE.  
SQ SEQUENCE 835 AA; 93336 MW; 94C9685F95C4A646 CRC64;

Query Match 53.4%; Score 47; DB 2; Length 835;  
Best Local Similarity 62.5%; Pred. No. 60;  
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 LRAGFYAVSFLSVAVG 19  
DB 527 LRAGVKNISLLSIAGV 542

RESULT 14  
AAF21626 PRELIMINARY; PRT; 835 AA.  
AC AAF21626;  
DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
DE Beta-galactosidase precursor.  
GN TEG1.  
OS Lycopersicon esculentum (Tomato).  
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;  
OC Solanales; Solanaceae; Solanum.  
OX NCBI\_TaxID=4081;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV. Rutgers; TISSUE=fruit;  
RX MEDLINE=98289087; PubMed=9625694;  
RA Smith D.L., Starratt D.A., Gross K.C.;  
RT "A gene coding for tomato fruit beta-galactosidase II is expressed during fruit ripening. Cloning, characterization, and expression pattern."  
RT Plant Physiol. 117:417-423(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV. Rutgers; TISSUE=fruit;  
RA Smith D.L., Gross K.C.;  
RT "A family of at least seven beta-galactosidase genes is expressed during tomato fruit development."  
RL Plant Physiol. 123:1173-1183(2000).  
DR EMBL; AF023847; AAF21626.1; -  
KW Signal.

FT SIGNAL 1 22 POTENTIAL.  
FT CHAIN 23 835 BETA-GALACTOSIDASE.  
SQ SEQUENCE 835 AA; 93336 MW; 94C9685F95C4A646 CRC64;

Query Match 53.4%; Score 47; DB 2; Length 835;  
Best Local Similarity 62.5%; Pred. No. 60;  
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 LRAGFYAVSFLSVAVG 19  
DB 527 LRAGVKNISLLSIAGV 542

RESULT 15  
Q9ZP11 PRELIMINARY; PRT; 838 AA.  
AC Q9ZP11;  
DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE SS-galactosidase precursor (EC 3.2.1.23).  
GN Name=regIA;  
OS Lycopersicon esculentum (Tomato).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Magnoliophyta; eudicotyledons; core eudicots; asterids;  
OC Lamiales; Solanales; Solanaceae; Solanum.  
OX NCBI\_TaxID=4081;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA De Silva J., Jarman C., Strongitharm B., Gidley M.;  
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.  
CC -1- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing beta-D-galactose residues in beta-D-galactosides.  
CC -1- SIMILARITY: Belongs to family 35 of glycosyl hydrolases.  
DR EMBL; AJ012796; CAA10173.1; -  
DR GO; GO:0009341; C:beta-galactosidase complex; IEA.  
DR GO; GO:0004565; F:beta-galactosidase activity; IEA.  
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.  
DR GO; GO:0005529; F:sugar binding; IEA.  
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
DR InterPro; IPR008979; Gal\_bind like.  
DR InterPro; IPR008922; Gal\_lectin.  
DR InterPro; IPR001944; Glyco\_hydro\_35.  
DR Pfam; PF02140; Gal\_lectin; 1.  
DR Pfam; PF01301; Glyco\_hydro\_35; 1.  
DR PRINTS; PR00742; GLHYDRLASE35.  
DR PRODOM; PD005612; Gal\_lectin; 1.  
DR PROSITE; PS01182; GLYCOSYL\_HYDROL\_F35; 1.  
DR PROSITE; PS0228; SUEL\_LECTIN; 1.  
KW Glycosidase; Hydrolase; Signal.  
FT SIGNAL 1 25  
FT CHAIN 26 838 ss-galactosidase.  
SQ SEQUENCE 838 AA; 92923 MW; AC2E11ABFA417762 CRC64;

Query Match 53.4%; Score 47; DB 2; Length 838;  
Best Local Similarity 62.5%; Pred. No. 60;  
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 LRAGFYAVSFLSVAVG 19  
DB 530 LRAGVKNISLLSIAGV 545

Search completed: November 16, 2004, 19:14:33  
Job time : 24.4175 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 16, 2004, 17:12:10 ; Search time 20.2095 Seconds  
(without alignments)  
337.259 Million cell updates/sec

Title: US-10-036-444-5

Perfect score: 88

Sequence: 1 VLLLRAGFYAVSPLSVAVG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*

- 1: Geneseq1980s:\*
- 2: Geneseq1990s:\*
- 3: Geneseq2000s:\*
- 4: Geneseq2001s:\*
- 5: Geneseq2002s:\*
- 6: Geneseq2003as:\*
- 7: Geneseq2003bs:\*
- 8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	88	100.0	19	4	Aae02772 Human Nkp
2	88	100.0	19	8	Adq30925 Human Nkp
3	88	100.0	177	2	Aay06402 Human B-C
4	88	100.0	190	2	Aay06401 Human B-C
5	88	100.0	190	4	Aae02769 Human Nkp
6	88	100.0	190	8	Ado19810 Human PRO
7	88	100.0	190	8	Adq30923 Human Nkp
8	88	100.0	201	2	Aay06403 Human B-C
9	80	90.9	19	5	Aae02772 Human Nkp
10	51	58.0	274	3	Aag23590 Arabidops
11	51	58.0	279	3	Aag23589 Arabidops
12	48	54.5	665	6	Aao16046 Carica pa
13	48	54.5	665	6	Aae32202 Papaya be
14	48	54.5	721	6	Aao16048 Carica pa
15	48	54.5	721	6	Aae32204 Papaya be
16	47	53.4	835	3	Aay44303 Tomato be
17	47	53.4	838	2	Aar2882 Tomato ex
18	47	53.4	838	3	Aay44305 Tomato be
19	46	52.3	114	3	AAG05624 Arabidops
20	46	52.3	119	3	AAG05623 Arabidops
21	46	52.3	127	3	AAG05622 Arabidops
22	46	52.3	651	3	AAG42606 Arabidops
23	46	52.3	714	3	AAG42605 Arabidops
24	46	52.3	724	3	Aay44306 Tomato be
25	46	52.3	757	3	Aag42604 Arabidops

26	46	52.3	757	5	AB991980	Ab91980 Herbicida
27	45	51.1	1563	6	ABU41824	Abu41824 Protein e
28	44	50.0	87	7	ADC97632	Adc97632 E. faeciu
29	44	50.0	385	7	AA320910	Aab20910 Drosophil
30	44	50.0	385	7	AD215306	Add15306 Fruitfly
31	44	50.0	417	4	AA81928	Aag81928 S. epider
32	44	50.0	425	5	ABP66312	Abp66312 Bifidobac
33	44	50.0	602	5	ABP39571	Abp39571 Staphyloc
34	44	50.0	602	6	ABU42891	Abu42891 Protein e
35	43.5	49.4	355	7	ADJ69975	Adj69975 Human hea
36	43.5	49.4	383	6	ABO00770	Ab000770 Polypepti
37	43	48.9	154	6	ABO00816	Ab000816 Polypepti
38	43	48.9	166	4	AB866413	Ab866413 Drosophil
39	43	48.9	469	4	AA376682	Aab76682 Corynebac
40	43	48.9	530	4	AA376681	Aab76681 Corynebac
41	43	48.9	530	4	AA379761	Adg79761 Corynebac
42	43	48.9	536	7	ADG74257	Adg74257 Fruit fly
43	43	48.9	578	4	AA90808	Aag90808 C glutami
44	43	48.9	589	4	AB871245	Ab871245 Drosophil
45	42	47.7	271	6	ABU35719	Abu35719 Protein e

#### ALIGNMENTS

##### RESULT 1

AAE02772

ID AAE02772 standard; peptide; 19 AA.

XX

AC AAE02772;

XX

DT 06-AUG-2001 (first entry)

XX

DE Human Nkp30 receptor transmembrane region sequence.

XX

KW Human; Nkp30 receptor; natural killer cell; cytostatic; antimicrobial;  
KW melanoma; hepatocarcinoma; lung adenocarcinoma; viral infection; tumour;  
KW immunosuppressant; antiviral; drug; grafting enhancement; leukaemia;  
KW therapy; transmembrane region.

XX

OS Homo sapiens.

XX

FN WO200136630-A2.

XX

PD 25-MAY-2001.

XX

PF 15-NOV-2000; 2000WO-EP011697.

XX

PR 15-NOV-1999; 99CA-02288307.

PR

15-NOV-1999; 99US-00440514.

XX

PA (INNA-) INNATE PHARMA SAS.

PA

(UYGE-) UNIV GENOVA.

XX

PI Moretta A, Bottino C, Biassoni R;

XX

WPI; 2001-329221/34.

XX

DR Novel compound, useful for detection and/or quantifying the presence of

XX

PT NK cells, comprises the amino acid sequences of the Nkp30 molecule.

XX

PS Claim 1; Fig 7B; 83pp; English.

XX

CC The invention relates to human Nkp30 receptor and its corresponding cDNA  
CC molecule which is involved in natural cytotoxicity mediated by natural  
CC killer (NK) cells and antibodies that identify the same Nkp30 receptor  
CC is a member of immunoglobulin super family (Ig-SF). Nkp30 is selectively  
CC expressed on the surface of human mature NK cells. Nkp30 is selectively  
CC useful for detecting and/or quantifying the presence of NK cells in a  
CC biological sample. The invention also provide kits for detecting and/or  
CC quantifying the presence of NK cells, for the selective removal of NK  
CC cells from a biological sample, for the positive and selective  
CC purification of NK cells from a biological sample and for the in vitro

CC stimulation of NK cell cytotoxicity. The invention further provides a  
CC pharmaceutical composition which is used as a drug for grafting  
CC enhancement, graft versus host (GVH) inhibition, stimulation of graft  
CC versus tumour (GVT) and especially graft versus leukaemia (GVL), and for  
CC the prevention, palliation and/or therapy of solid or liquid tumours,  
CC such as melanoma, hepatocarcinoma and lung adenocarcinoma, and/or  
CC microorganism, notably viral infection. NKp30 antibodies are useful for  
CC identifying NKp30 natural ligands and allow assessment of the level of  
CC surface NKp30 ligand expressed on an NK-susceptible target cell and the  
CC comparison of this level to the standard physiological one. Hence NKp30  
CC antibodies are useful in the diagnosis of tumours or of infection. The  
CC present sequence is the transmembrane region of human NKp30 receptor  
XX  
XX  
SQ Sequence 19 AA;

Query Match 100.0%; Score 88; DB 4; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.9e-08;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLLRAGFYAVSFSLVAVG 19  
DB 1 VLLLRAGFYAVSFSLVAVG 19

RESULT 2  
ADQ30925  
ID ADQ30925 standard; protein; 19 AA.  
AC ADQ30925;  
XX  
XX 23-SEP-2004 (first entry)  
XX Human NKp30 transmembrane region.  
XX Natural killer cell; NK cell; NKp30; cytostatic; antimicrobial.

XX Homo sapiens.  
XX WO2004056392-A1.  
XX 08-JUL-2004.  
XX 22-DEC-2003; 2003WO-EP014716.  
XX 23-DEC-2002; 2002US-0435344P.  
XX (INNA-) INNATE PHARMA.  
XX Romagne F, Andre P;  
XX WPI; 2004-507595/48.  
XX  
XX Pharmaceutical compositions that stimulate proliferation of natural  
XX killer cells useful for therapy of melanoma, chronic myeloid, and  
XX leukemia, comprise an anti-natural killer cell receptor antibody and  
XX interleukins.  
XX  
XX Claim 3; SEQ ID NO 3; 35pp; English.

XX The present sequence is that of the transmembrane region of human NKp30  
XX ADQ30923, a 190 amino acid polypeptide that is selectively expressed by  
XX natural killer (NK) cells, and particularly by mature NK cells. Claimed  
XX pharmaceutical compositions that have a stimulating effect on the  
XX proliferation of NK cells comprise an antibody such as an anti-NKp30  
XX antibody or anti-NKp46 antibody or its immuno-reactive fragment and a  
XX cytokine selected from interleukin-2 (IL2), IL12, IL15 and IL21, the  
XX antibody(ies) and cytokine(s) being administered together or separately  
XX to a subject. The anti-NKp30 antibody is an isolated antibody or its  
XX antigen-binding fragment which specifically binds to NKp30 or to a  
XX fragment, including the transmembrane region, of NKp30. The  
XX pharmaceutical compositions, when used for daily subcutaneous injection,  
XX comprising from 1 ng to 100 mg/kg (body weight) of antibody(ies), and  
XX lower than 1 million units/square meters/day of cytokine(s), are useful

CC for the prevention, palliation and therapy of e.g. melanoma, chronic  
CC myeloid leukaemia, acute myeloid leukaemia, lymphoma, multiple myeloma,  
CC hepatocarcinoma, lung adenocarcinoma, neuroblastoma and for antimicrobial  
CC prevention, palliation and therapy (claimed).  
XX  
SQ Sequence 19 AA;

Query Match 100.0%; Score 88; DB 8; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.9e-08;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLLRAGFYAVSFSLVAVG 19  
DB 1 VLLLRAGFYAVSFSLVAVG 19

RESULT 3  
AA06402  
ID AA06402 standard; protein; 177 AA.  
XX  
XX AC AA06402;  
XX  
XX 20-SEP-1999 (first entry)  
XX Human B-cell myelin oligodendrocyte glycoprotein BMOG.  
XX  
XX MBOG; B-cell myelin oligodendrocyte glycoprotein; human;  
XX signal transduction; immunomodulator; antiinflammatory;  
XX autoimmune disease; inflammation; gene therapy; diagnosis.  
XX Homo sapiens.

XX Key Location/Qualifiers  
XX Peptide 1..12  
XX Protein /note= "leader peptide"  
XX /note= "mature protein"  
XX Modified-site 42  
XX /note= "N-glycosylated"  
XX Modified-site 58  
XX /note= "N-glycosylated"  
XX Modified-site 121  
XX /note= "N-glycosylated"  
XX Domain 139..162  
XX /note= "transmembrane domain"  
XX Peptide 166..177  
XX /note= "alternatively spliced C-terminal end"

XX WO9223867-A2.  
XX  
XX 20-MAY-1999.  
XX  
XX 05-NOV-1998; 98WO-US023826.  
XX  
XX 07-NOV-1997; 97US-0064761P.  
XX  
XX (BIOJ) BIOGEN INC.  
XX  
XX Browning J;  
XX  
XX WPI; 1999-418423/35.  
XX N-PSDB; AAX59348.  
XX  
XX Novel B-cell myelin oligodendrocyte glycoproteins.  
XX  
XX Claim 2; Page 43; 43pp; English.

XX This sequence represents human BMOG, a novel member of the B cell myelin  
XX oligodendrocyte glycoprotein family that is expressed by germinal centre  
XX B cells. 3 C-terminal splice variants (see AA06401-03) of BMOG were  
XX identified. The protein is present primarily in the spleen, in lymph  
XX nodes and in germinal centre B cells. It may have immunoregulatory  
XX functions, and soluble or chimeric fusion proteins of BMOG may be used to

CC regulate the immune system in autoimmune or inflammatory disease. Vectors  
 CC comprising BMOG, prokaryotic and eukaryotic host cells, and a method of  
 CC producing BMOG using these transformed host cells are also provided. BMOG  
 CC polypeptides can be used for modulating the immune system of a subject or  
 CC to inhibit signal transduction in a cell expressing BMOG by contacting it  
 CC with a soluble BMOG protein. The nucleic acid can be used for gene  
 CC therapy. The protein can also be used to target a toxin, imaging agent or  
 CC radionuclide to a cell expressing BMOG. (All claimed)

XX Sequence 177 AA;

Query Match 100.0%; Score 88; DB 2; Length 177;  
 Best Local Similarity 100.0%; Pred. No. 7.7e-07;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLLRAGFYAVSFLSVAVG 19  
 DB 139 VLLLRAGFYAVSFLSVAVG 157

RESULT 4  
 ID AAY06401  
 AC AAY06401;  
 XX 20-SEP-1999 (first entry)  
 XX Human B-cell myelin oligodendrocyte glycoprotein BMOG.  
 XX MBOG; B-cell myelin oligodendrocyte glycoprotein; human;  
 KW signal transduction; immunomodulator; antiinflammatory;  
 KW autoimmune disease; inflammation; gene therapy; diagnosis.  
 XX Homo sapiens.

Key	Location/Qualifiers
FT Peptide	1..12 /note= "leader peptide"
FT Protein	13..190 /note= "mature protein"
FT Modified-site	42 /note= "N-glycosylated"
FT Modified-site	68 /note= "N-glycosylated"
FT Modified-site	121 /note= "N-glycosylated"
FT Domain	139..162 /note= "transmembrane domain"
FT Peptide	165..190 /note= "alternatively spliced C-terminal end"

XX WO9923867-A2.

XX 20-MAY-1999.

XX 05-NOV-1998; 98WO-US023826.

XX 07-NOV-1997; 97US-0064761P.

XX (BIOJ) BIOGEN INC.

XX Browning J;

XX WPI; 1999-418423/35.

XX N-PSDB; AAX59347.

XX Novel B-cell myelin oligodendrocyte glycoproteins.

XX Claim 2; Page 42; 43pp; English.

XX This sequence represents human BMOG, a novel member of the B cell myelin  
 CC oligodendrocyte glycoprotein family that is expressed by germinal centre

CC B cells. 3 C-terminal splice variants (see AAY06401-03) of BMOG were  
 CC identified. The protein is present primarily in the spleen, in lymph  
 CC nodes and in germinal centre B cells. It may have immunoregulatory  
 CC functions, and soluble or chimeric fusion proteins of BMOG may be used to  
 CC regulate the immune system in autoimmune or inflammatory disease. Vectors  
 CC comprising BMOG, prokaryotic and eukaryotic host cells, and a method of  
 CC producing BMOG using these transformed host cells are also provided. BMOG  
 CC polypeptides can be used for modulating the immune system of a subject or  
 CC to inhibit signal transduction in a cell expressing BMOG by contacting it  
 CC with a soluble BMOG protein. The nucleic acid can be used for gene  
 CC therapy. The protein can also be used to target a toxin, imaging agent or  
 CC radionuclide to a cell expressing BMOG. (All claimed)

XX Sequence 190 AA;

Query Match 100.0%; Score 88; DB 2; Length 190;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-07;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLLRAGFYAVSFLSVAVG 19  
 DB 139 VLLLRAGFYAVSFLSVAVG 157

RESULT 5

AAE02769  
 ID AAE02769 standard; protein; 190 AA.

XX AAE02769;

XX 06-AUG-2001 (first entry)

XX Human Nkp30 receptor.

KW Human; Nkp30 receptor; natural killer cell; cytostatic; antimicrobial;  
 KW melanoma; hepatocarcinoma; lung adenocarcinoma; viral infection; tumour;  
 KW immunosuppressant; antiviral; drug; grafting enhancement; leukaemia;  
 KW therapy.

XX Homo sapiens.

Key	Location/Qualifiers
FT Peptide	1..18 /label= "Signal_peptide"
FT Protein	19..190 /label= "Mature_Nkp30_receptor_protein"
FT Region	19..138 /label= "Extracellular_region"
FT Modified-site	42 /note= "Forms an immunoglobulin (Ig) V-like domain"
FT Modified-site	121 /note= "N-glycosylation site"
FT Region	139..157 /note= "N-glycosylation site"
FT Region	158..190 /label= "Transmembrane_region"
FT Region	158..190 /label= "Intracellular_region"

XX WO200136630-A2.

XX 25-MAY-2001.

XX 15-NOV-2000; 2000WO-EP011697.

XX 15-NOV-1999; 99CA-02288307.

XX 15-NOV-1999; 99US-00440514.

XX (INNA-) INNATE PHARMA SAS.

XX (UYGE-) UNIV GENOVA.

XX Moretta A, Bottino C, Biassoni R;

XX WPI; 2001-329221/34.

DR N-PSDB; AAD06564.  
 XX Novel compound, useful for detection and/or quantifying the presence of  
 PT NK cells, comprises the amino acid sequences of the Nkp30 molecule.  
 XX  
 PS Claim 1; Fig 7B; 83pp; English.  
 XX  
 CC The invention relates to human Nkp30 receptor and its corresponding cDNA  
 CC molecule which is involved in natural cytotoxicity mediated by natural  
 CC killer (NK) cells and antibodies that identify the same. Nkp30 is selectively  
 CC is a member of immunoglobulin super family (Ig-SF). Nkp30 is selectively  
 CC expressed on the surface of human mature NK cells. Nkp30 and its cDNA are  
 CC useful for detecting and/or quantifying the presence of NK cells in a  
 CC biological sample. The invention also provide kits for detecting and/or  
 CC quantifying the presence of NK cells, for the selective removal of NK  
 CC cells from a biological sample, for the positive and selective  
 CC purification of NK cells from a biological sample and for the in vitro  
 CC stimulation of NK cell cytotoxicity. The invention further provides a  
 CC pharmaceutical composition which is used as a drug for grafting  
 CC enhancement, graft versus host (GvH) inhibition, stimulation of graft  
 CC versus tumour (GvT) and especially graft versus leukaemia (GvL), and for  
 CC the prevention, palliation and/or therapy of solid or liquid tumours,  
 CC such as melanoma, hepatocarcinoma and lung adenocarcinoma, and/or  
 CC microorganism, notably viral infection. Nkp30 antibodies are useful for  
 CC identifying Nkp30 natural ligands and allow assessment of the level of  
 CC surface Nkp30 ligand expressed on an NK-susceptible target cell and the  
 CC comparison of this level to the standard physiological one. Hence Nkp30  
 CC antibodies are useful in the diagnosis of tumours or of infection. The  
 CC present sequence is human Nkp30 receptor  
 XX  
 SQ Sequence 190 AA;  
 Query Match 100.0%; Score 88; DB 4; Length 190;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-07;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VLLLRAGFYAVSFLSVAVG 19  
 Db 139 VLLLRAGFYAVSFLSVAVG 157  
 RESULT 6  
 ID ADO19810 standard; protein; 190 AA.  
 XX ADO19810;  
 AC ADO19810;  
 DT 12-AUG-2004 (first entry)  
 XX Human PRO polypeptide #367.  
 DE Human; PRO; immune related disorder; systemic lupus erythematosus;  
 XX rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;  
 KW systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;  
 KW autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;  
 KW diabetes mellitus; renal disease; demyelinating disease;  
 KW central nervous system; peripheral nervous system;  
 KW demyelinating polyneuropathy; Guillain-Barre syndrome;  
 KW chronic inflammatory demyelinating polyneuropathy.  
 XX Homo sapiens.  
 OS WO2004043361-A2.  
 PN 27-MAY-2004.  
 PD 06-NOV-2003; 2003WO-US035268.  
 PF 08-NOV-2002; 2002US-0425235P.  
 PR (GETH ) GENENTECH INC.  
 XX Forq S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;  
 PI

PI Wood WI, Wu TD;  
 XX WPI; 2004-420067/39.  
 DR N-PSDB; ADO19809.  
 XX  
 PT Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for  
 PT treating an immune related disorder such as systemic lupus erythematosus,  
 PT rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or  
 PT spondyloarthritis.  
 XX  
 PS Claim 7; SEQ ID NO 734; 1731pp; English.  
 XX  
 CC The invention relates to human PRO polypeptides and the polynucleotides  
 CC encoding them. The polypeptides and polynucleotides are useful for  
 CC treating and diagnosing immune related disorders in mammals. The immune  
 CC related disorders include systemic lupus erythematosus, rheumatoid  
 CC arthritis, Sjogren's syndrome, juvenile chronic arthritis, systemic  
 CC sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune  
 CC haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes  
 CC mellitus, immune-mediated renal disease, demyelinating diseases of the  
 CC central or peripheral nervous system, demyelinating polyneuropathy,  
 CC Guillain-Barre syndrome and chronic inflammatory demyelinating  
 CC polyneuropathy. This sequence represents a human PRO polypeptide of the  
 CC invention.  
 XX  
 SQ Sequence 190 AA;  
 Query Match 100.0%; Score 88; DB 8; Length 190;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-07;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VLLLRAGFYAVSFLSVAVG 19  
 Db 139 VLLLRAGFYAVSFLSVAVG 157  
 RESULT 7  
 ID ADO30923 standard; protein; 190 AA.  
 XX ADO30923;  
 AC ADO30923;  
 DT 23-SEP-2004 (first entry)  
 XX Human Nkp30 polypeptide.  
 DE Human Nkp30 polypeptide.  
 KW Natural killer cell; NK cell; Nkp30; cytostatic; antimicrobial.  
 XX Homo sapiens.  
 OS  
 FH Key Location/Qualifiers  
 FT Region 19..138  
 FT /label= Extracellular region  
 FT /note= "Region specifically described in Claim 3"  
 FT Region 20..33  
 FT /label  
 FT /note= "Immunogenic peptide specifically described in  
 FT Claim 3"  
 FT Region 139..157  
 FT /label= Transmembrane region  
 FT /note= "Region specifically described in Claim 3"  
 FT Region 158..190  
 FT /label= Cytoplasmic tail  
 FT /note= "Region specifically described in Claim 3"  
 XX WO2004056392-A1.  
 PN 08-JUL-2004.  
 PD 22-DEC-2003; 2003WO-EF014716.  
 PF 23-DEC-2002; 2002US-0435344P.  
 PR



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PA (INNA-) INNATE PHARMA.
XX
XX Romagne F, Andre P;
XX WPI; 2004-507595/48.
XX
XX Pharmaceutical compositions that stimulate proliferation of natural
XX killer cells useful for therapy of melanoma, chronic myeloid, and
XX leukemia, comprise an anti-natural killer cell receptor antibody and
XX interleukins.
XX
XX Claim 3; SEQ ID NO 1; 35pp; English.
XX
XX The present sequence is that of human NKP30, a 190 amino acid polypeptide
XX (about 30 kDa on SDS-PAGE) that is selectively expressed by natural
XX killer (NK) cells, and particularly by mature NK cells. Claimed
XX pharmaceutical compositions that have a stimulating effect on the
XX proliferation of NK cells comprise an antibody such as an anti-NKP30
XX antibody or anti-NKP46 antibody or its immuno-reactive fragment and a
XX cytokine selected from interleukin-2 (IL2), IL12, IL15 and IL21, the
XX antibody(ies) and cytokine(s) being administered together or separately
XX to a subject. The anti-NKP30 antibody is an isolated antibody or its
XX antigen-binding fragment which specifically binds to NKP30 or to a
XX fragment ADQ10924-ADQ10927 of NKP30. The pharmaceutical compositions,
XX when used for daily subcutaneous injection, comprising from 1 ng to 100
XX mg/kg (body weight) of antibody(ies), and lower than 1 million
XX units/square meters/day of cytokine(s), are useful for the prevention,
XX palliation and therapy of e.g. melanoma, chronic myeloid leukaemia, acute
XX myeloid leukaemia, lymphoma, multiple myeloma, hepatocarcinoma, lung
XX adenocarcinoma, neuroblastoma and for antimicrobial prevention,
XX palliation and therapy (Claimed).
XX
XX Sequence 190 AA;
XX
XX Query Match 100.0%; Score 88; DB 8; Length 190;
XX Best Local Similarity 100.0%; Pred. No. 8.4e-07;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLLLRAGFYAVSFLSVAVG 19
Db 139 VLLLRAGFYAVSFLSVAVG 157

RESULT 8
AA06403
ID AA06403 standard; protein; 201 AA.
AC AA06403;
XX
XX 20-SEP-1999 (first entry)
XX
XX Human B-cell myelin oligodendrocyte glycoprotein BMOG.
XX
XX BMOG; B-cell myelin oligodendrocyte glycoprotein; human;
XX signal transduction; immunomodulator; antiinflammatory;
XX autoimmune disease; inflammation; gene therapy; diagnosis.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..12
XX /note= "leader peptide"
XX Protein 13..201
XX /note= "mature protein"
XX Modified-site 42
XX /note= "N-glycosylated"
XX Modified-site 68
XX /note= "N-glycosylated"
XX Modified-site 121
XX /note= "N-glycosylated"
XX Domain 139..162
XX /note= "transmembrane domain"
XX Peptide 166..201

/INNA-/) INNATE PHARMA.
/alternatively spliced C-terminal end"
WO9923867-A2.
20-MAY-1999.
05-NOV-1998; 98WO-US023826.
07-NOV-1997; 97US-0064761P.
(BIOJ ) BIOGEN INC.
Browning J;
WPI; 1999-418423/35.
N-PSDB; AAX59349.
Novel B-cell myelin oligodendrocyte glycoproteins.
Claim 2; Page 43; 43pp; English.
This sequence represents human BMOG, a novel member of the B cell myelin
oligodendrocyte glycoprotein family that is expressed by germinal centre
B cells. 3 C-terminal splice variants (see AAY06401-03) of BMOG were
identified. The protein is present primarily in the spleen, in lymph
nodes and in germinal centre B cells. It may have immunoregulatory
functions, and soluble or chimeric fusion proteins of BMOG may be used to
regulate the immune system in autoimmune or inflammatory disease. Vectors
comprising BMOG, prokaryotic and eukaryotic host cells, and a method of
producing BMOG using these transformed host cells are also provided. BMOG
polypeptides can be used for modulating the immune system of a subject or
to inhibit signal transduction in a cell expressing BMOG by contacting it
with a soluble BMOG protein. The nucleic acid can be used for gene
therapy. The protein can also be used to target a toxin, imaging agent or
radionuclide to a cell expressing BMOG. (All claimed)
XX
XX Sequence 201 AA;
XX
XX Query Match 100.0%; Score 88; DB 2; Length 201;
XX Best Local Similarity 100.0%; Pred. No. 8.9e-07;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLLLRAGFYAVSFLSVAVG 19
Db 139 VLLLRAGFYAVSFLSVAVG 157

RESULT 9
AAE23900
ID AAE23900 standard; peptide; 19 AA.
AC AAE23900;
XX
XX 10-SEP-2002 (first entry)
XX
XX Human NKP30 receptor peptide.
XX
XX KAR-associated protein; KARAP-transduced immune signal; dendritic cell;
XX antigen presentation; contact sensitivity; multiple sclerosis;
XX neuroprotective; human; NKP30 receptor peptide.
XX
XX Homo sapiens.
XX
XX WO200224940-A2.
XX
XX 28-MAR-2002.
XX
XX 20-SEP-2001; 2001WO-EP011492.
XX
XX 20-SEP-2000; 2000US-0234161P.
XX
XX (INRM ) INSRM INST NAT SANTE & RECH MEDICALE.
XX

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PI Vivier E, Vely F, Tomasello E;
XX WPI; 2002-454420/48.
XX
XX
XX Identifying KAR-associated protein-transduced immune signal inhibitor,
PT comprises using cells co-expressing functional KARAP, and engineered
PT cells and animals that over-express functional KARAP or bear non-
PT functional KARAP.
XX
XX Example 4; Page 45; 89pp; English.
XX
XX The present invention relates to a novel method for identifying compounds
CC capable of inhibiting KAR-associated protein (KARAP)-transduced immune
CC signals. The method involves using functional and non-functional KARAP,
CC cells co-expressing functional KARAP, functional receptors transducing
CC their signal by zeta, gamma or epsilon and engineered cells and animals
CC over-expressing functional KARAP or bearing non-functional KARAP. The
CC method is useful for identifying compounds capable of inhibiting KARAP-
CC transduced immune signals. The KARAP-inhibiting compounds are useful for
CC impairing the development and maturation of dendritic cells, for
CC inhibiting the antigen presentation of dendritic cells, for synthesis
CC inhibition or through inhibition of the migration of dendritic cells, for
CC making drugs intended for inhibiting dendritic cell development or
CC maturation, for preparing drugs for the treatment, prevention, palliation
CC of immune response, where the activation of KAR has to be inhibited and
CC for the treatment of contact sensitivity or multiple sclerosis. The
CC present sequence is human NKp30 receptor peptide which associate with CD3
CC zeta and FcR gamma. This sequence is used in the exemplification of the
CC invention
XX
XX Sequence 19 AA;
XX
XX Query Match 90.9%; Score 80; DB 5; Length 19;
XX Best Local Similarity 100.0%; Pred. NO. 1.4e-06;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 3 LLRAGFYAVSFLSVAVG 19
XX |||||
XX 1 LLRAGFYAVSFLSVAVG 17
XX
XX RESULT 10
XX AAG23590
XX ID AAG23590 standard; protein; 274 AA.
XX
XX AC AAG23590;
XX
XX DT 17-OCT-2000 (first entry)
XX
XX XX Arabidopsis thaliana protein fragment SEQ ID NO: 26954.
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX
XX OS Arabidopsis thaliana.
XX
XX PN EP1033405-A2.
XX
XX PD 06-SEP-2000.
XX
XX PP 25-FEB-2000; 2000EP-00301439.
XX
XX PR 25-FEB-1999; 99US-0121825P.
XX PR 05-MAR-1999; 99US-0123180P.
XX PR 05-MAR-1999; 99US-01233548P.
XX PR 23-MAR-1999; 99US-0125788P.
XX PR 23-MAR-1999; 99US-0126264P.
XX PR 23-MAR-1999; 99US-0126785P.
XX PR 01-APR-1999; 99US-0127462P.
XX PR 06-APR-1999; 99US-0128234P.
XX PR 08-APR-1999; 99US-0128714P.
XX PR 16-APR-1999; 99US-0129845P.
XX
XX PR 19-APR-1999; 99US-0130077P.
XX PR 21-APR-1999; 99US-0130449P.
XX PR 23-APR-1999; 99US-0130510P.
XX PR 23-APR-1999; 99US-0130891P.
XX PR 28-APR-1999; 99US-0131449P.
XX PR 30-APR-1999; 99US-0132048P.
XX PR 30-APR-1999; 99US-0132407P.
XX PR 04-MAY-1999; 99US-0132484P.
XX PR 05-MAY-1999; 99US-0132485P.
XX PR 06-MAY-1999; 99US-0132486P.
XX PR 06-MAY-1999; 99US-0132487P.
XX PR 07-MAY-1999; 99US-0132863P.
XX PR 11-MAY-1999; 99US-0134256P.
XX PR 14-MAY-1999; 99US-0134218P.
XX PR 14-MAY-1999; 99US-0134219P.
XX PR 14-MAY-1999; 99US-0134221P.
XX PR 14-MAY-1999; 99US-0134370P.
XX PR 18-MAY-1999; 99US-0134768P.
XX PR 19-MAY-1999; 99US-0134941P.
XX PR 20-MAY-1999; 99US-0135124P.
XX PR 21-MAY-1999; 99US-0135333P.
XX PR 24-MAY-1999; 99US-0135629P.
XX PR 25-MAY-1999; 99US-0136021P.
XX PR 27-MAY-1999; 99US-0136392P.
XX PR 28-MAY-1999; 99US-0136782P.
XX PR 01-JUN-1999; 99US-0137222P.
XX PR 03-JUN-1999; 99US-0137528P.
XX PR 04-JUN-1999; 99US-0137502P.
XX PR 07-JUN-1999; 99US-0137724P.
XX PR 08-JUN-1999; 99US-0138094P.
XX PR 10-JUN-1999; 99US-0138540P.
XX PR 10-JUN-1999; 99US-0138847P.
XX PR 14-JUN-1999; 99US-0139119P.
XX PR 16-JUN-1999; 99US-0139452P.
XX PR 16-JUN-1999; 99US-0139453P.
XX PR 17-JUN-1999; 99US-0139452P.
XX PR 18-JUN-1999; 99US-0139454P.
XX PR 18-JUN-1999; 99US-0139455P.
XX PR 18-JUN-1999; 99US-0139456P.
XX PR 18-JUN-1999; 99US-0139457P.
XX PR 18-JUN-1999; 99US-0139458P.
XX PR 18-JUN-1999; 99US-0139459P.
XX PR 18-JUN-1999; 99US-0139460P.
XX PR 18-JUN-1999; 99US-0139461P.
XX PR 18-JUN-1999; 99US-0139462P.
XX PR 18-JUN-1999; 99US-0139463P.
XX PR 18-JUN-1999; 99US-0139750P.
XX PR 18-JUN-1999; 99US-0139763P.
XX PR 21-JUN-1999; 99US-0139817P.
XX PR 22-JUN-1999; 99US-0139899P.
XX PR 23-JUN-1999; 99US-0140353P.
XX PR 23-JUN-1999; 99US-0140354P.
XX PR 24-JUN-1999; 99US-0140635P.
XX PR 28-JUN-1999; 99US-0140823P.
XX PR 29-JUN-1999; 99US-0140931P.
XX PR 30-JUN-1999; 99US-0141287P.
XX PR 01-JUL-1999; 99US-0141842P.
XX PR 01-JUL-1999; 99US-0142154P.
XX PR 02-JUL-1999; 99US-0142055P.
XX PR 06-JUL-1999; 99US-0142330P.
XX PR 08-JUL-1999; 99US-0142803P.
XX PR 09-JUL-1999; 99US-0142920P.
XX PR 12-JUL-1999; 99US-0142977P.
XX PR 13-JUL-1999; 99US-0143542P.
XX PR 14-JUL-1999; 99US-0143624P.
XX PR 15-JUL-1999; 99US-0144005P.
XX PR 16-JUL-1999; 99US-0144085P.
XX PR 16-JUL-1999; 99US-0144086P.
XX PR 19-JUL-1999; 99US-0144325P.
XX PR 19-JUL-1999; 99US-0144331P.
XX PR 19-JUL-1999; 99US-0144332P.
XX PR 19-JUL-1999; 99US-0144333P.
XX PR 19-JUL-1999; 99US-0144334P.

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PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0146389P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147132P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151085P.
PR 27-AUG-1999; 99US-0151086P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155113P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157855P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.
PR 29-OCT-1999; 99US-0162143P.

Query Match 58.0%; Score 51; DB 3; Length 274;
Best Local Similarity 62.5%; Fred. No. 2.7;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 LRAGFYAVSF*LSVAVG 19
    ||||| : : : : :
Db 30 LRAGENKIALLSIAGV 45

RESULT 11
AAG23589
ID AAG23589 standard; protein; 279 AA.
XX AC AAG23589;
XX AC AAG23589;
DT 17-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 26953.
XX KW Protein identification; signal transduction pathway; metabolic pathway;
XX KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX KW termination sequence.
XX OS Arabidopsis thaliana.
XX EP1033405-A2.
PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-00301439.
XX 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125789P.
PR 29-MAR-1999; 99US-0126264P.
PR 01-APR-1999; 99US-0126785P.
PR 06-APR-1999; 99US-0127462P.
PR 08-APR-1999; 99US-0128234P.
PR 16-APR-1999; 99US-0128714P.
PR 19-APR-1999; 99US-0129845P.
PR 21-APR-1999; 99US-0130077P.
PR 23-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 28-APR-1999; 99US-0130891P.
PR 30-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
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PR 21-OCT-1999; 99US-0160768P.  
 PR 21-OCT-1999; 99US-0160770P.  
 PR 21-OCT-1999; 99US-0160814P.  
 PR 21-OCT-1999; 99US-0160815P.  
 PR 22-OCT-1999; 99US-0160800P.  
 PR 22-OCT-1999; 99US-0160981P.  
 PR 22-OCT-1999; 99US-0160981P.  
 PR 22-OCT-1999; 99US-0160989P.  
 PR 25-OCT-1999; 99US-0161404P.  
 PR 25-OCT-1999; 99US-0161405P.  
 PR 25-OCT-1999; 99US-0161406P.  
 PR 26-OCT-1999; 99US-0161359P.  
 PR 26-OCT-1999; 99US-0161360P.  
 PR 26-OCT-1999; 99US-0161361P.  
 PR 28-OCT-1999; 99US-0161920P.  
 PR 28-OCT-1999; 99US-0161922P.  
 PR 28-OCT-1999; 99US-0161933P.  
 PR 29-OCT-1999; 99US-0162142P.

Query Match 58.0%; Score 51; DB 3; Length 279;  
 Best Local Similarity 62.5%; Pred. No. 2.7;  
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 LRAGFYAVSFSLVAVG 19  
 ||||| : : : : :  
 Db 35 LRAGFNKIALISIAVG 50

RESULT 12  
 AAO16046  
 ID AAO16046 standard; protein; 665 AA.

XX AAO16046;  
 XX  
 DT 27-FEB-2003 (first entry)  
 XX  
 DE Carica papaya beta-galactosidase (Beta-gal-45).  
 XX  
 KW Enzyme; papaya; beta-galactosidase; pectinmethylesterase;  
 KW polygalacturonase; fruit ripening.  
 XX

OS Carica papaya.

XX WO200283924-A2.

XX 24-OCT-2002.

XX 11-APR-2002; 2002WO-US011804.

XX 11-APR-2001; 2001US-0283008P.

XX (CORR ) CORNELL RES FOUND INC.

XX (PAIS/) PAIS M S S.

XX Pais MSS, Gonsalves D, Balde A;

XX WPI; 2003-075556/07.

XX N-PSDB; AAL51072.

XX New isolated nucleic acid molecule encoding beta-galactosidase protein,  
 useful for promoting or delaying papaya fruit ripening.

XX Claim 3; Page 9-13; 84pp; English.

XX The invention comprises the amino acid and coding sequence of Carica  
 CC papaya beta-galactosidase proteins which control papaya fruit ripening.  
 CC The invention also comprises the amino acid and coding sequence of Carica  
 CC papaya pectinmethylesterase and polygalacturonase proteins. The DNA and  
 CC protein sequences of the invention are useful for promoting or delaying  
 CC papaya fruit ripening. The present amino acid sequence represents a  
 CC Carica papaya fruit ripening-related protein of the invention

XX Sequence 665 AA;

Query Match 54.5%; Score 48; DB 6; Length 665;  
 Best Local Similarity 62.5%; Pred. No. 24;  
 Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 LRAGFYAVSFSLVAVG 19  
 ||||| : : : : :  
 Db 383 LRAGINKISLSIAVG 398

RESULT 13  
 AAE32202  
 ID AAE32202 standard; protein; 665 AA.

XX AAE32202;

XX 24-MAR-2003 (first entry)

XX Papaya beta-galactosidase (beta-Gal).45.

XX Fruit ripening; papaya ringspot virus coat protein; transgenic plant;  
 KW transgenic; PRSV; CP; beta-galactosidase; beta-Gal.45; enzyme.

XX Carica papaya.

XX Key Location/Qualifiers

FT Misc-difference 143

FT /label= Unknown

FT /note= "Encoded by TGN"

XX WO200282889-A1.

XX 24-OCT-2002.

XX 11-APR-2002; 2002WO-US011803.

XX 11-APR-2001; 2001US-0283022P.

XX (CORR ) CORNELL RES FOUND INC.

XX (PAIS/) PAIS M S S.

XX Pais MSS, Gonsalves D, Balde A, Chiang C;

XX WPI; 2003-075493/07.

XX N-PSDB; AAD49832.

XX New DNA construct, useful for controlling the ripening of papaya fruit  
 PT and conferring resistance to papaya ringspot virus coat in transgenic  
 PT plants.

XX Disclosure; Page 75-77; 121pp; English.

XX The invention relates to a DNA construct comprising a first DNA molecule  
 CC encoding a protein that controls papaya fruit ripening and a second DNA  
 CC molecule encoding a papaya ringspot virus (PRSV) coat protein (CP). The  
 CC DNA construct is useful for controlling the ripening of papaya fruit and  
 CC conferring resistance to PRSV coat in transgenic plants. The present  
 CC sequence is papaya beta-galactosidase (beta-Gal).45

XX Sequence 665 AA;

Query Match 54.5%; Score 48; DB 6; Length 665;  
 Best Local Similarity 62.5%; Pred. No. 24;  
 Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 LRAGFYAVSFSLVAVG 19  
 ||||| : : : : :  
 Db 383 LRAGINKISLSIAVG 398

RESULT 14  
 AAO16048  
 ID AAO16048 standard; protein; 721 AA.

XX

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AC AAO16048;
XX
XX 27-FEB-2003 (first entry)
XX
XX Carica papaya beta-galactosidase (Beta-gal-41).
XX
XX Enzyme; papaya; beta-galactosidase; pectinmethylesterase;
XX polygalacturonase; fruit ripening.
XX
XX Carica papaya.
XX
XX WO200283924-A2.
XX
XX 24-OCT-2002.
XX
XX 11-APR-2002; 2002WO-US011804.
XX
XX 11-APR-2001; 2001US-0283008P.
XX
XX (CORR ) CORNELL RES FOUND INC.
XX (PAIS/) PAIS M S S.
XX
XX Pals MSS, Gonsalves D, Balde A;
XX
XX WPI; 2003-075556/07.
XX N-PSDB; AALS1074.
XX
XX New isolated nucleic acid molecule encoding beta-galactosidase protein,
XX useful for promoting or delaying papaya fruit ripening.
XX
XX Claim 17; Page 15-19; 84pp; English.
XX
XX The invention comprises the amino acid and coding sequence of Carica
XX papaya beta-galactosidase proteins which control papaya fruit ripening.
XX The invention also comprises the amino acid and coding sequence of Carica
XX papaya pectinmethylesterase and polygalacturonase proteins. The DNA and
XX protein sequences of the invention are useful for promoting or delaying
XX papaya fruit ripening. The present amino acid sequence represents a
XX Carica papaya fruit ripening-related protein of the invention
XX
XX SQ Sequence 721 AA;
XX
XX Query Match 54.5%; Score 48; DB 6; Length 721;
XX Best Local Similarity 68.8%; Pred. No. 26;
XX Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 4 LRAGFYAVSFSLVAVG 19
XX ||||| |||||
XX 526 LRAGVNVKVSLLSIAGV 541
XX
XX Db
XX
XX RESULT 15
XX AAE32204
XX ID AAE32204 standard; protein; 721 AA.
XX
XX AC AAE32204;
XX
XX 24-MAR-2003 (first entry)
XX
XX Papaya beta-galactosidase (beta-Gal).41.
XX
XX Fruit ripening; papaya ringspot virus coat protein; transgenic plant;
XX transgenic; PRSV; CP; beta-galactosidase; beta-Gal.41; enzyme.
XX
XX Carica papaya.
XX
XX WO200282889-A1.
XX
XX 24-OCT-2002.
XX
XX 11-APR-2002; 2002WO-US011803.
XX
XX 11-APR-2001; 2001US-0283022P.
XX
XX PR

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XX (CORR ) CORNELL RES FOUND INC.
XX (PAIS/) PAIS M S S.
XX
XX Pals MSS, Gonsalves D, Balde A, Chiang C;
XX
XX WPI; 2003-075493/07.
XX N-PSDB; AAD49834.
XX
XX New DNA construct, useful for controlling the ripening of papaya fruit
XX and conferring resistance to papaya ringspot virus coat in transgenic
XX plants.
XX
XX Disclosure; Page 80-83; 121pp; English.
XX
XX The invention relates to a DNA construct comprising a first DNA molecule
XX encoding a protein that controls papaya fruit ripening and a second DNA
XX molecule encoding a papaya ringspot virus (PRSV) coat protein (CP). The
XX DNA construct is useful for controlling the ripening of papaya fruit and
XX conferring resistance to PRSV coat in transgenic plants. The present
XX sequence is papaya beta-galactosidase (beta-Gal).41
XX
XX SQ Sequence 721 AA;
XX
XX Query Match 54.5%; Score 48; DB 6; Length 721;
XX Best Local Similarity 68.8%; Pred. No. 26;
XX Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 4 LRAGFYAVSFSLVAVG 19
XX ||||| |||||
XX 526 LRAGVNVKVSLLSIAGV 541
XX
XX Db
XX
XX Search completed: November 16, 2004, 18:55:58
XX Job time : 24.2095 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 16, 2004, 19:14:52 : Search time 16.9841 Seconds  
(without alignments)  
395.815 Million cell updates/sec

Title: US-10-036-444-5

Perfect score: 88

Sequence: 1 VLLLRAGFYAVSFLSVAVG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1568699 seqs, 353819137 residues

Total number of hits satisfying chosen parameters: 1568699

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pap:
- 2: /cgn2\_6/ptodata/1/pubpaa/PCR\_NEW\_PUB.pap:
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pap:
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pap:
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pap:
- 6: /cgn2\_6/ptodata/1/pubpaa/PCRUS\_PUBCOMB.pap:
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pap:
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pap:
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pap:
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pap:
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pap:
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pap:
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pap:
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pap:
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pap:
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pap:
- 17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pap:
- 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pap:
- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pap:
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	88	100.0	19	13 US-10-036-444-5	Sequence 5, Appli
2	88	100.0	161	16 US-10-696-259-10	Sequence 10, Appl
3	88	100.0	175	16 US-10-696-259-8	Sequence 8, Appli
4	88	100.0	177	16 US-10-696-259-5	Sequence 5, Appli
5	88	100.0	185	16 US-10-696-259-7	Sequence 7, Appli
6	88	100.0	190	13 US-10-036-444-2	Sequence 2, Appli
7	88	100.0	190	16 US-10-696-259-4	Sequence 4, Appli
8	88	100.0	198	16 US-10-696-259-9	Sequence 9, Appli
9	88	100.0	201	16 US-10-696-259-6	Sequence 6, Appli
10	49	55.7	100	16 US-10-437-963-161934	Sequence 161934,
11	48	54.5	428	15 US-10-424-599-207360	Sequence 207360,
12	48	54.5	665	14 US-10-121-393-2	Sequence 2, Appli
13	48	54.5	665	14 US-10-121-539-2	Sequence 2, Appli

14	48	54.5	721	14	US-10-121-393-6	Sequence 6, Appli
15	48	54.5	721	14	US-10-121-539-6	Sequence 6, Appli
16	45	51.1	231	17	US-10-425-115-349552	Sequence 349552,
17	45	51.1	250	15	US-10-425-114-48020	Sequence 48020, A
18	45	51.1	1563	15	US-10-282-122A-69748	Sequence 69748, A
19	44.5	50.6	473	14	US-10-369-493-10510	Sequence 10510, A
20	44	50.0	222	15	US-10-425-114-55971	Sequence 55971, A
21	44	50.0	247	15	US-10-425-114-40659	Sequence 40659, A
22	44	50.0	312	15	US-10-425-114-49039	Sequence 49039, A
23	44	50.0	385	15	US-10-601-309-20	Sequence 20, Appl
24	44	50.0	392	15	US-10-425-114-43621	Sequence 43621, A2
25	44	50.0	433	15	US-10-425-114-36786	Sequence 36786, A
26	44	50.0	493	15	US-10-424-599-246507	Sequence 246507,
27	44	50.0	523	15	US-10-424-599-236336	Sequence 236336,
28	44	50.0	602	15	US-10-282-122A-70815	Sequence 70815, A
29	44	50.0	727	15	US-10-425-114-52764	Sequence 52764, A
30	44	50.0	727	15	US-10-425-114-55408	Sequence 55408, A
31	44	50.0	739	15	US-10-424-599-262939	Sequence 262939,
32	43.5	49.4	355	16	US-10-408-765A-1781	Sequence 1781, Ap
33	43	48.9	154	14	US-10-243-552-940	Sequence 940, App
34	43	48.9	361	17	US-10-739-930-10917	Sequence 10917, A
35	43	48.9	469	15	US-10-627-476-346	Sequence 346, App
36	43	48.9	530	15	US-10-627-476-344	Sequence 344, App
37	43	48.9	536	10	US-09-847-102A-42	Sequence 42, Appl
38	43	48.9	578	9	US-09-738-626-4562	Sequence 4562, Ap
39	42	47.7	65	15	US-10-424-599-242117	Sequence 242117,
40	42	47.7	87	15	US-10-437-963-154905	Sequence 154905,
41	42	47.7	271	15	US-10-282-122A-63643	Sequence 63643, A
42	42	47.7	388	15	US-10-389-647-564	Sequence 564, App
43	42	47.7	914	16	US-10-437-963-131538	Sequence 131538,
44	41.5	47.2	566	15	US-10-287-226-300	Sequence 300, App
45	41.5	47.2	589	9	US-09-740-041-2	Sequence 2, Appli

#### ALIGNMENTS

##### RESULT 1

US-10-036-444-5  
; Sequence 5, Application US/10036444  
; Publication No. US20020142445A1  
; GENERAL INFORMATION:  
; APPLICANT: INNATE PHARMA S.A.S.  
; TITLE OF INVENTION: UNIVERSITA DI GENOVA  
; TITLE OF INVENTION: cytotoxicity mediated by human Natural Killer cells and  
; TITLE OF INVENTION: antibodies that identify the same"  
; FILE REFERENCE: SEQ-FR-1060  
; CURRENT APPLICATION NUMBER: US/10/036.444  
; PRIOR FILING DATE: 2002-01-07  
; PRIOR APPLICATION NUMBER: 09/440,514  
; PRIOR FILING DATE: 1999-11-15  
; PRIOR APPLICATION NUMBER: 09/456,199  
; PRIOR FILING DATE: 1999-12-07  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Human NK cell  
US-10-036-444-5

Query Match 100.0%; Score 88; DB 13; Length 19;  
Best Local Similarity 100.0%; Pred. No. 9.9e-08;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLLLRAGFYAVSFLSVAVG 19

Db 1 VLLLRAGFYAVSFLSVAVG 19

##### RESULT 2

US-10-696-259-10

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; Sequence 10, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapien
; US-10-696-259-10

Query Match      100.0%; Score 88; DB 16; Length 161;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLLRAGFYAVSFSLVAVG 19
Db 138 VLLLRAGFYAVSFSLVAVG 156

RESULT 3
US-10-696-259-8
; Sequence 8, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Homo sapien
; US-10-696-259-8

Query Match      100.0%; Score 88; DB 16; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLLRAGFYAVSFSLVAVG 19
Db 137 VLLLRAGFYAVSFSLVAVG 155

RESULT 4
US-10-696-259-5
; Sequence 5, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo sapien
; US-10-696-259-5

Query Match      100.0%; Score 88; DB 16; Length 177;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLLRAGFYAVSFSLVAVG 19
Db 139 VLLLRAGFYAVSFSLVAVG 157

RESULT 5
US-10-696-259-7
; Sequence 7, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapien
; US-10-696-259-7

Query Match      100.0%; Score 88; DB 16; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLLRAGFYAVSFSLVAVG 19
Db 137 VLLLRAGFYAVSFSLVAVG 155

RESULT 6
US-10-036-444-2
; Sequence 2, Application US/10036444
; Publication No. US20020142445A1
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; GENERAL INFORMATION:
; APPLICANT: INNATE PHARMA S.A.S.
; TITLE OF INVENTION: "No. US20020142445A1el triggering receptor involved in natural
; TITLE OF INVENTION: cytotoxicity mediated by human Natural Killer cells and
; TITLE OF INVENTION: antibodies that identify the same"
; FILE REFERENCE: SEQ-PR-1060
; CURRENT APPLICATION NUMBER: US/10/036,444
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 09/440,514
; PRIOR FILING DATE: 1999-11-15
; PRIOR APPLICATION NUMBER: 09/456,199
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Human NK cell
US-10-036-444-2

Query Match      100.0%; Score 88; DB 13; Length 190;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VLLLRAGFYAVSFLSVAVG 19
      |||||
Db      139 VLLLRAGFYAVSFLSVAVG 157

RESULT 7
US-10-696-259-4
; Sequence 4, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-4

Query Match      100.0%; Score 88; DB 16; Length 190;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VLLLRAGFYAVSFLSVAVG 19
      |||||
Db      139 VLLLRAGFYAVSFLSVAVG 157

RESULT 8
US-10-696-259-9
; Sequence 9, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-6

Query Match      100.0%; Score 88; DB 16; Length 201;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VLLLRAGFYAVSFLSVAVG 19
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Db      139 VLLLRAGFYAVSFLSVAVG 157

RESULT 9
US-10-696-259-6
; Sequence 6, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-6

Query Match      100.0%; Score 88; DB 16; Length 201;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VLLLRAGFYAVSFLSVAVG 19
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Db      139 VLLLRAGFYAVSFLSVAVG 157

RESULT 10
US-10-437-963-161934
; Sequence 161934, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
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; PRIOR FILING DATE: 2001-04-11
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Carica papaya
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (143)
; OTHER INFORMATION: Xaa at position 143 in this sequence is any amino
; OTHER INFORMATION: acid
US-10-121-393-2

Query Match          54.5%; Score 48; DB 14; Length 665;
Best Local Similarity 62.5%; Pred.No.23;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      4  LRAGFYAVSFSLVAVG 19
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Db      383  LRAINKISLSIAVG 398

RESULT 13
US-10-121-539-2
; Sequence 2, Application US/10121539
; Publication No. US20030204869A1
; GENERAL INFORMATION:
; APPLICANT: Gonsalves, Dennis
; APPLICANT: Balde, Aladjé
; APPLICANT: Pais, Maria Salome Soares
; APPLICANT: Chiang, Chu-Hui
; TITLE OF INVENTION: A METHOD TO CONTROL THE RIPENING OF PAPAYA FRUIT AND
; TITLE OF INVENTION: CONFER DISEASE RESISTANCE TO PAPAYA PLANTS
; FILE REFERENCE: 19603/3601
; CURRENT APPLICATION NUMBER: US/10/121,539
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 60/283,022
; PRIOR FILING DATE: 2001-04-11
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO. 2
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Carica papaya
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (143)
; OTHER INFORMATION: Xaa at position 143 in this sequence is any amino
; OTHER INFORMATION: acid
US-10-121-539-2

Query Match          54.5%; Score 48; DB 14; Length 665;
Best Local Similarity 62.5%; Pred.No.23;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      4  LRAGFYAVSFSLVAVG 19
      ||||| : |||: |||
Db      383  LRAINKISLSIAVG 398

RESULT 14
US-10-121-393-6
; Sequence 6, Application US/10121393
; Publication No. US20030115633A1
; GENERAL INFORMATION:
; APPLICANT: Pais, Marie Salome Soares
; APPLICANT: Gonsalves, Dennis
; APPLICANT: Balde, Aladjé
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES RELATING TO PAPAYA RIPENING
; FILE REFERENCE: 19603/3001
; CURRENT APPLICATION NUMBER: US/10/121,393
; CURRENT FILING DATE: 2002-04-11

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; PRIOR APPLICATION NUMBER: 60/283,008  
; PRIOR FILING DATE: 2001-04-11  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 721  
; TYPE: PRT  
; ORGANISM: Carica papaya  
US-10-121-393-6

Query Match 54.5%; Score 48; DB 14; Length 721;  
Best Local Similarity 68.8%; Pred. No. 26;  
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 4 LRAGFYAVSFLSIVAG 19  
Db 526 LRAGVNVSVLSIIVAG 541

RESULT 15  
US-10-121-539-6  
; Sequence 6, Application US/10121539  
; Publication No. US20030204869A1  
; GENERAL INFORMATION:  
; APPLICANT: Gonsalves, Dennis  
; APPLICANT: Balde, Aladje  
; APPLICANT: Pais, Maria Salome Soares  
; APPLICANT: Chiang, Chu-Hui  
; TITLE OF INVENTION: A METHOD TO CONTROL THE RIPENING OF PAPAYA FRUIT AND  
; TITLE OF INVENTION: CONFER DISEASE RESISTANCE TO PAPAYA PLANTS  
; FILE REFERENCE: 19603/3601  
; CURRENT APPLICATION NUMBER: US/10/121,539  
; CURRENT FILING DATE: 2002-04-11  
; PRIOR APPLICATION NUMBER: 60/283,022  
; PRIOR FILING DATE: 2001-04-11  
; NUMBER OF SEQ ID NOS: 90  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 721  
; TYPE: PRT  
; ORGANISM: Carica papaya  
US-10-121-539-6

Query Match 54.5%; Score 48; DB 14; Length 721;  
Best Local Similarity 68.8%; Pred. No. 26;  
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 4 LRAGFYAVSFLSIVAG 19  
Db 526 LRAGVNVSVLSIIVAG 541

Search completed: November 16, 2004, 19:45:05  
Job time : 17.9841 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2004, 19:05:01 ; Search time 63.2493 Seconds  
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332.841 Million cell updates/sec

Title: US-10-036-444-5

Perfect score: 88  
Sequence: 1 VLLLRAGFYAVSFLSVAVG 19

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Gapop 10.0 , Gapext 0.5

Searched: 6730630 seqs, 1107998698 residues

Total number of hits satisfying chosen parameters: 6730630

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	88	100.0	19	18	US-09-456-199-5
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4	88	100.0	152	22	US-09-791-537-140678
5	88	100.0	161	19	US-09-560-855A-10
6	88	100.0	161	32	US-10-696-259-10
7	88	100.0	165	22	US-09-791-537-140916
8	88	100.0	175	19	US-09-560-855A-8
9	88	100.0	175	32	US-10-696-259-8
10	88	100.0	176	22	US-09-791-537-141562
11	88	100.0	177	19	US-09-560-855-5
12	88	100.0	177	19	US-09-560-855A-5
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16	88	100.0	177	36	US-60-443-566-3830
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18	88	100.0	177	36	US-60-455-444-8478
19	88	100.0	177	36	US-60-465-241-8478
20	88	100.0	185	19	US-09-560-855A-7
21	88	100.0	185	32	US-10-696-259-7
22	88	100.0	190	18	US-09-440-514-2
23	88	100.0	190	18	US-09-456-199-2
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25	88	100.0	190	19	US-09-560-855A-4
26	88	100.0	190	26	US-10-036-444-2
27	88	100.0	190	27	US-10-170-2058-32498
28	88	100.0	190	32	US-10-696-259-4
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30	88	100.0	190	36	US-60-452-680-24531
31	88	100.0	190	36	US-60-455-444-8476
32	88	100.0	190	36	US-60-465-241-8476
33	88	100.0	198	19	US-09-560-855A-9
34	88	100.0	198	32	US-10-696-259-9
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45	88	100.0	231	22	US-09-760-476-1763

#### ALIGNMENTS

#### RESULT 1

US-09-440-514-5  
; Sequence 5, Application US/09440514  
; GENERAL INFORMATION:  
; APPLICANT: INNATE PHARMA S.A.S.  
; APPLICANT: UNIVERSITA DI GENOVA  
; TITLE OF INVENTION: "Novel triggering receptor involved in natural  
; TITLE OF INVENTION: cytotoxicity mediated by human Natural Killer cells and  
; FILE REFERENCE: SEQ-FR-1060  
; CURRENT APPLICATION NUMBER: US/09440,514  
; CURRENT FILING DATE: 1999-11-15  
; PRIOR APPLICATION NUMBER: 09/456,199  
; PRIOR FILING DATE: 1999-12-07  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Human NK cell

## US-09-440-514-5

Query Match 100.0%; Score 88; DB 18; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 5.6e-06;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLLLRAGFYAVSFSLVAVG 19  
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 Db 1 VLLLRAGFYAVSFSLVAVG 19

## RESULT 2

US-09-456-199-5  
 ; Sequence 5, Application US/09456199  
 ; GENERAL INFORMATION:  
 ; APPLICANT: INNATE PHARMA S.A.S.  
 ; APPLICANT: UNIVERSITA DI GENOVA  
 ; TITLE OF INVENTION: "Novel triggering receptor involved in natural  
 ; TITLE OF INVENTION: cytotoxicity mediated by human Natural Killer cells and  
 ; TITLE OF INVENTION: antibodies that identify the same"  
 ; FILE REFERENCE: SEQ-FR-1060  
 ; CURRENT APPLICATION NUMBER: US/09/456.199  
 ; CURRENT FILING DATE: 1999-12-07  
 ; NUMBER OF SEQ ID NOS: 13  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 5  
 ; LENGTH: 19  
 ; TYPE: PRT  
 ; ORGANISM: Human NK cell  
 US-09-456-199-5

Query Match 100.0%; Score 88; DB 18; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 5.6e-06;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLLLRAGFYAVSFSLVAVG 19  
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 Db 1 VLLLRAGFYAVSFSLVAVG 19

## RESULT 3

US-10-036-444-5  
 ; Sequence 5, Application US/10036444  
 ; GENERAL INFORMATION:  
 ; APPLICANT: INNATE PHARMA S.A.S.  
 ; APPLICANT: UNIVERSITA DI GENOVA  
 ; TITLE OF INVENTION: "Novel triggering receptor involved in natural  
 ; TITLE OF INVENTION: cytotoxicity mediated by human Natural Killer cells and  
 ; TITLE OF INVENTION: antibodies that identify the same"  
 ; FILE REFERENCE: SEQ-FR-1060  
 ; CURRENT APPLICATION NUMBER: US/10/036.444  
 ; CURRENT FILING DATE: 2002-01-07  
 ; PRIOR APPLICATION NUMBER: 09/440.514  
 ; PRIOR FILING DATE: 1999-11-15  
 ; PRIOR APPLICATION NUMBER: 09/456.199  
 ; PRIOR FILING DATE: 1999-12-07  
 ; NUMBER OF SEQ ID NOS: 13  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 5  
 ; LENGTH: 19  
 ; TYPE: PRT  
 ; ORGANISM: Human NK cell  
 US-10-036-444-5

Query Match 100.0%; Score 88; DB 26; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 5.6e-06;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLLLRAGFYAVSFSLVAVG 19  
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 Db 1 VLLLRAGFYAVSFSLVAVG 19

## RESULT 4

US-09-537-140678  
 ; Sequence 140678, Application US/09791537  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bionomix, Inc.  
 ; APPLICANT: Debe, Derek  
 ; APPLICANT: Danzer, Joseph  
 ; TITLE OF INVENTION: THREE-DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE  
 ; TITLE OF INVENTION: METHODS OF USE THEREOF  
 ; FILE REFERENCE: 261/210  
 ; CURRENT APPLICATION NUMBER: US/09/791.537  
 ; CURRENT FILING DATE: 2001-02-22  
 ; NUMBER OF SEQ ID NOS: 153055  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 140678  
 ; LENGTH: 152  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-537-140678

Query Match 100.0%; Score 88; DB 22; Length 152;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-05;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLLLRAGFYAVSFSLVAVG 19  
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## RESULT 5

US-09-560-855A-10  
 ; Sequence 10, Application US/09560855A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BIOGEN, INC  
 ; APPLICANT: BROWNING, Jeffrey  
 ; TITLE OF INVENTION: BMOG, A Novel Protein Member of the  
 ; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for  
 ; TITLE OF INVENTION: Immunomodulatory Purposes  
 ; FILE REFERENCE: A041 US  
 ; CURRENT APPLICATION NUMBER: US/09/560.855A  
 ; CURRENT FILING DATE: 2000-04-28  
 ; PRIOR APPLICATION NUMBER: PCT/US98/23826  
 ; PRIOR FILING DATE: 1998-11-05  
 ; PRIOR APPLICATION NUMBER: 60/064761  
 ; PRIOR FILING DATE: 1997-11-07  
 ; NUMBER OF SEQ ID NOS: 20  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 10  
 ; LENGTH: 161  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapien  
 US-09-560-855A-10

Query Match 100.0%; Score 88; DB 19; Length 161;  
 Best Local Similarity 100.0%; Pred. No. 4e-05;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLLLRAGFYAVSFSLVAVG 19  
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 Db 138 VLLLRAGFYAVSFSLVAVG 156

## RESULT 6

US-10-696-259-10  
 ; Sequence 10, Application US/10696259  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BIOGEN, INC  
 ; APPLICANT: BROWNING, Jeffrey  
 ; TITLE OF INVENTION: BMOG, A Novel Protein Member of the  
 ; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for  
 ; TITLE OF INVENTION: Immunomodulatory Purposes  
 ; FILE REFERENCE: A041 US  
 ; CURRENT APPLICATION NUMBER: US/10/696.259

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; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-696-259-10
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Query Match 100.0%; Score 88; DB 32; Length 161;
Best Local Similarity 100.0%; Pred. No. 4e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 VLLLRAGFYAVSFLSVAVG 19
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Db 138 VLLLRAGFYAVSFLSVAVG 156
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US-09-791-537-140916
; Sequence 140916, Application US/09/791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 140916
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-140916
```

```
Query Match 100.0%; Score 88; DB 22; Length 165;
Best Local Similarity 100.0%; Pred. No. 4e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VLLLRAGFYAVSFLSVAVG 19
| | | | | | | | | | | | | | | | | | | | | |
Db 114 VLLLRAGFYAVSFLSVAVG 132
```

## RESULT 8

```
US-09-560-855A-8
; Sequence 8, Application US/09560855A
; GENERAL INFORMATION:
; APPLICANT: BIONOMIX, INC.
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/09/560,855A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 175
```

```
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-560-855A-8
```

```
Query Match 100.0%; Score 88; DB 19; Length 175;
Best Local Similarity 100.0%; Pred. No. 4.3e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VLLLRAGFYAVSFLSVAVG 19
| | | | | | | | | | | | | | | | | | | | | |
Db 137 VLLLRAGFYAVSFLSVAVG 155
```

## RESULT 9

```
US-10-696-259-8
; Sequence 8, Application US/10696259
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-8
```

```
Query Match 100.0%; Score 88; DB 32; Length 175;
Best Local Similarity 100.0%; Pred. No. 4.3e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VLLLRAGFYAVSFLSVAVG 19
| | | | | | | | | | | | | | | | | | | | | |
Db 137 VLLLRAGFYAVSFLSVAVG 155
```

## RESULT 10

```
US-09-791-537-141562
; Sequence 141562, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 141562
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-141562
```

```
Query Match 100.0%; Score 88; DB 22; Length 176;
Best Local Similarity 100.0%; Pred. No. 4.3e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VLLLRAGFYAVSFLSVAVG 19
```

Db 114 VLLLRAGFYAVSFLSVAVG 132  
|||||

RESULT 11  
US-09-560-855-5  
; Sequence 5, Application US/09560855  
; GENERAL INFORMATION:  
; APPLICANT: Biogen, Inc.  
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the  
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use  
; TITLE OF INVENTION: For Immunomodulatory Purposes  
; FILE REFERENCE: A041PCT  
; CURRENT APPLICATION NUMBER: US/09/560,855  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: 60/064761  
; PRIOR FILING DATE: 1997-11-07  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 177  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-560-855-5

Query Match 100.0%; Score 88; DB 19; Length 177;  
Best Local Similarity 100.0%; Pred. No. 4.3e-05;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 VLLLRAGFYAVSFLSVAVG 19  
|||||

Db 139 VLLLRAGFYAVSFLSVAVG 157  
|||||

RESULT 12  
US-09-560-855A-5  
; Sequence 5, Application US/09560855A  
; GENERAL INFORMATION:  
; APPLICANT: BIOGEN, INC  
; APPLICANT: BROWNING, Jeffrey  
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the  
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for  
; TITLE OF INVENTION: Immunomodulatory Purposes  
; FILE REFERENCE: A041 US  
; CURRENT APPLICATION NUMBER: US/09/560,855A  
; CURRENT FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: PCT/US98/23826  
; PRIOR FILING DATE: 1998-11-05  
; PRIOR APPLICATION NUMBER: 60/064761  
; PRIOR FILING DATE: 1997-11-07  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 177  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-560-855A-5

Query Match 100.0%; Score 88; DB 19; Length 177;  
Best Local Similarity 100.0%; Pred. No. 4.3e-05;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 VLLLRAGFYAVSFLSVAVG 19  
|||||

Db 139 VLLLRAGFYAVSFLSVAVG 157  
|||||

RESULT 13  
US-09-791-537-140612  
; Sequence 140612, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek

; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE  
; TITLE OF INVENTION: METHODS OF USE THEREOF  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537.  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 140612  
; LENGTH: 177  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-791-537-140612

Query Match 100.0%; Score 88; DB 22; Length 177;  
Best Local Similarity 100.0%; Pred. No. 4.3e-05;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 VLLLRAGFYAVSFLSVAVG 19  
|||||

Db 139 VLLLRAGFYAVSFLSVAVG 157  
|||||

RESULT 14  
US-10-170-205E-32655  
; Sequence 32655, Application US/10170205E  
; GENERAL INFORMATION:  
; APPLICANT: ADAMS, Mark  
; TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN  
; TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF  
; FILE REFERENCE: CLOC1381  
; CURRENT APPLICATION NUMBER: US/10/170,205E  
; CURRENT FILING DATE: 2002-06-13  
; NUMBER OF SEQ ID NOS: 40312  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 32655  
; LENGTH: 177  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-170-205E-32655

Query Match 100.0%; Score 88; DB 27; Length 177;  
Best Local Similarity 100.0%; Pred. No. 4.3e-05;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 VLLLRAGFYAVSFLSVAVG 19  
|||||

Db 139 VLLLRAGFYAVSFLSVAVG 157  
|||||

RESULT 15  
US-10-696-259-5  
; Sequence 5, Application US/10696259  
; GENERAL INFORMATION:  
; APPLICANT: BIOGEN, INC  
; APPLICANT: BROWNING, Jeffrey  
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the  
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for  
; TITLE OF INVENTION: Immunomodulatory Purposes  
; FILE REFERENCE: A041 US  
; CURRENT APPLICATION NUMBER: US/10/696,259  
; CURRENT FILING DATE: 2003-10-28  
; PRIOR APPLICATION NUMBER: US/09/560,855A  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: PCT/US98/23826  
; PRIOR FILING DATE: 1998-11-05  
; PRIOR APPLICATION NUMBER: 60/064761  
; PRIOR FILING DATE: 1997-11-07  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 177  
; TYPE: PRT



; ORGANISM: Homo sapien  
US-10-696-259-5

Query Match 100.0%; Score 88; DB 32; Length 177;  
Best Local Similarity 100.0%; Pred. No. 4.3e-05;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLLLRAGFYAVSFSLVAVG 19  
| | | | | | | | | | | | | | | | | | | | |  
Db 139 VLLLRAGFYAVSFSLVAVG 157

Search completed: November 16, 2004, 19:38:44  
Job time : 63.2493 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
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OM protein - protein search, using 'sw model

Run on: November 16, 2004, 18:56:40 ; Search time 6.82759 Seconds  
(without alignments)  
465.048 Million cell updates/sec

Title: US-10-036-444-6

Perfect score: 204

Sequence: 1 STVYQKCHCHMGTHCHSSDGRGVIPRCP 33

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 791\*

1: PIR1:\*

2: PIR2:\*

3: PIR3:\*

4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	60	29.4	1801	1 MMRTS	laminin beta-2 cha
2	59.5	29.2	660	1 QMBE3	BHLPI protein - hu
3	59	28.9	544	2 T3645	probable large int
4	58.5	28.7	116	2 T46473	hypothetical prote
5	58	28.4	180	2 E84768	hypothetical prote
6	57	27.9	435	2 S40993	hypothetical prote
7	56.5	27.7	1321	2 JE0352	mucin MUC5B, trach
8	55	27.0	1620	2 T27283	hypothetical prote
9	54.5	26.7	147	2 S37485	gene msgl protein
10	54.5	26.7	3078	2 T28432	variant-specific s
11	53.5	26.5	1300	2 A36302	insulin receptor-r
12	53	26.2	2767	1 UIHU	thrycoglobulin prec
13	53	26.0	460	2 D97679	argininosuccinate
14	53	26.0	597	2 T16006	protein kinase C3
15	52.5	25.7	91	2 S37486	gene msg3 protein
16	52.5	25.7	153	2 PN0564	von Willebrand fac
17	52.5	25.7	577	2 B37357	integrin beta-6 ch
18	52.5	25.7	799	2 A38308	integrin beta-5 ch
19	52	25.5	137	2 A87586	hypothetical prote
20	52	25.5	1798	2 S53869	laminin beta-2 cha
21	51.5	25.2	106	2 T48808	hypothetical prote
22	51.5	25.2	138	2 B95330	Hmr heavy metal d
23	51.5	25.2	378	2 B59180	Wnt inhibitory fac
24	51.5	25.2	435	2 T48724	hypothetical prote
25	51.5	25.2	436	2 D88826	protein lin-3 (imp
26	51.5	25.2	438	2 S28263	lin-3 protein prec
27	51.5	25.2	929	2 T51932	kinesin [imported]
28	51.5	25.2	1166	1 S06142	protein-tyrosine k
29	51.5	25.2	1344	2 S47412	gene P2 protein -

30	51	25.0	325	2 B43692	T2 protein - rabbi
31	51	25.0	434	1 A35005	u-plasminogen acti
32	50.5	24.8	106	2 B64350	hypothetical prote
33	50.5	24.8	247	2 T50874	hypothetical cytoc
34	50.5	24.8	515	2 T23089	hypothetical prote
35	50.5	24.8	656	2 JC2005	integrin beta-5 ch
36	50.5	24.8	677	2 H86208	protein F22G5.26 l
37	50.5	24.8	1111	2 T26972	hypothetical prote
38	50.5	24.8	1722	2 E89753	protein F11C7.4 [i
39	50	24.5	82	2 F68870	hypothetical prote
40	50	24.5	174	2 C48583	stress-inducible p
41	50	24.5	354	2 T22274	hypothetical prote
42	50	24.5	732	2 I52361	testicular metallo
43	50	24.5	5376	2 T42215	zonadhesin - mouse
44	49.5	24.3	1574	2 T13954	MEGF6 protein - ra
45	49.5	24.3	1914	2 T42635	tenascin V precurs

#### ALIGNMENTS

##### RESULT 1

##### MMRTS

laminin beta-2 chain precursor - rat

N:Alternate names: laminin chain B3; S-laminin

C:Species: Rattus norvegicus (Norway rat)

C>Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 09-Jul-2004

C:Accession: S03539

R:Hunter, D.D.; Shah, V.; Merlie, J.P.; Sanes, J.R.

Nature 338, 229-234, 1989

A:Title: A laminin-like adhesive protein concentrated in the synaptic cleft of the neur

A:Reference number: S03539; MUID:89159410; PMID:2922051

A:Accession: S03539

A:Molecule type: mRNA

A:Residues: 1-1801 <HUN>

A:Cross-references: UNIPROT:P15800; EMBL:X16563; NID:G57250; PIDN:CAA34561.1; PID:G5725

C:Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin

C:Function:

A:Description: interact with cells and with other basement membrane proteins to promote

C:Superfamily: laminin beta-1 chain; laminin-type EGF-like homology

C:Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular

F:1-35/Domain: signal sequence #status predicted <SIG>

F:36-1801/Product: laminin beta-2 chain #status predicted <MAT>

F:36-285/Domain: VI <DOM6>

F:286-555/Domain: V <DOM5>

F:286-347/Domain: laminin-type EGF-like homology <LE01>

F:350-410/Domain: laminin-type EGF-like homology <LE02>

F:413-470/Domain: laminin-type EGF-like homology <LE03>

F:473-522/Domain: laminin-type EGF-like homology <LE04>

F:525-555/Domain: laminin-type EGF-like homology #status atypical <LE05>

F:556-784/Domain: IV <DOM4>

F:786-831/Domain: laminin-type EGF-like homology <LE06>

F:788-1156/Domain: III <DOM3>

F:834-877/Domain: laminin-type EGF-like homology <LE07>

F:880-927/Domain: laminin-type EGF-like homology <LE08>

F:930-986/Domain: laminin-type EGF-like homology <LE09>

F:989-1038/Domain: laminin-type EGF-like homology <LE10>

F:1041-1095/Domain: laminin-type EGF-like homology <LE11>

F:1098-1143/Domain: laminin-type EGF-like homology <LE12>

F:1146-1190/Domain: laminin-type EGF-like homology <LE13>

F:1197-1412/Domain: II <DOM2>

F:1197-1412/Region: heptad repeats

F:1413-1445/Domain: alpha <ALP>

F:1446-1801/Region: heptad repeats

F:1446-1801/Domain: I <DOM1>

F:45-50/Disulfide bonds: #status predicted

F:251-371,1088,1252,1311,1351,1502/Binding site: carbohydrate (Asn) (covalent) #status 1

F:1197,1196,1800/Disulfide bonds: interchain #status predicted

Query Match 29.4%; Score 60; DB 1; Length 1801;

Best Local Similarity 29.8%; Pred. No. 21;

Matches 14; Conservative 5; Mismatches 8; Indels 20; Gaps 3;



JE0352  
mucin MUC5B, tracheobronchial - human  
C:Species: Homo sapiens (man)  
C:Date: 05-Feb-1999 #sequence\_revision 05-Feb-1999 #text\_change 21-Jul-2000  
C:Accession: JE0352  
R:Offner, G.D.; Nunes, D.P.; Keates, A.C.; Afdhal, N.H.; Troxler, R.F.  
Biochem. Biophys. Res. Commun. 251, 350-355, 1998  
A:Title: The amino-terminal sequence of MUC5B contains conserved multifunctional D domain  
A:Reference number: JE0352; MUID:99009274; PMID:9790959  
A:Accession: JE0352  
A:Molecule type: mRNA  
A:Residues: 1-1321 <OFF>  
A:Cross-references: GB:AF086604; NID:g3789926; PIDN:AAC67545.1; PID:g3789927  
C:Comment: This protein is large multimeric glycoproteins which is secreted by epithelia  
C:Genetics:  
A:Gene: MUC5B

Query Match 27.7%; Score 56.5; DB 2; Length 1321;  
Best Local Similarity 39.0%; Pred. No. 42;  
Matches 16; Conservative 0; Mismatches 10; Indels 15; Gaps 3;

QY 7 GKCH-----CHMGTHCHS-----SDGPRGVPEPRCP 33  
Db 816 GSCHTLDVGC-FSTHCVSGVCVCPPLVSDGSGGCIABEDCP 855

RESULT 8  
T27283  
hypothetical protein Y64G10A.f - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C:Accession: T27283  
R:Ainscough, R.  
submitted to the EMBL Data Library, September 1999  
A:Reference number: Z20336  
A:Accession: T27283  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-1620 <WIL>  
A:Cross-references: EMBL:AL110498; NID:e1542303; PIDN:CAB54471.1; CESP:Y64G10A.f  
A:Experimental source: clone Y64G10A  
C:Genetics:  
A:Gene: CESP:Y64G10A.f  
A:Introns: 77/1; 116/1; 198/1; 282/1; 365/1; 425/1; 466/1; 548/1; 559/1; 601/1; 625/1; 7

Query Match 27.0%; Score 55; DB 2; Length 1620;  
Best Local Similarity 46.2%; Pred. No. 78;  
Matches 12; Conservative 0; Mismatches 8; Indels 6; Gaps 1;

QY 8 KCHCHMGTHCHSDGPRGVPEPRCP 33  
Db 1012 KCDACDGMHCDPSDG-----ECICP 1031

RESULT 9  
S37485  
gene msg1 protein - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
C:Accession: I48669; S37485  
R:Tronik-Le Roux, D.; Senorale-Pose, M.; Rougeon, F.  
Gene 142, 175-182, 1994  
A:Title: Three novel SMK1-related cDNAs characterized in the submaxillary gland of mice  
A:Reference number: I48669; MUID:94252564; PMID:8194749  
A:Accession: I48669  
A:Status: preliminary;  
A:Molecule type: mRNA  
A:Residues: 1-147 <RES>  
A:Cross-references: UNIPROT:Q61900; EMBL:X71629; NID:g406256; PIDN:CAA50636.1; PID:g4062  
C:Genetics:  
A:Gene: msg1  
C:Superfamily: proline-rich peptide P-B

Query Match 26.7%; Score 54.5; DB 2; Length 147;  
Best Local Similarity 44.0%; Pred. No. 10;  
Matches 11; Conservative 0; Mismatches 11; Indels 3; Gaps 1;

QY 9 CHCHMGTHCHSDGPRGVPEPRCP 33  
Db 20 CECHGRPRHD---PRGFFPFPPPP 41

RESULT 10  
T28432  
variant-specific surface protein 1 - malaria parasite (Plasmodium falciparum)  
N:Alternate names: erythrocyte membrane binding protein 1 (EMP1)  
C:Species: Plasmodium falciparum  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T28432  
R:Su, X.Z.; Heatwole, V.M.; Wertheimer, S.P.; Guinet, F.; Herrfeldt, J.A.; Peterson, D.; Cell 82, 89-100, 1995  
A:Title: The large diverse gene family var encodes proteins involved in cytoadherence a  
A:Reference number: Z20487; MUID:95330613; PMID:7606788  
A:Accession: T28432  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-3078 <SUX>  
A:Cross-references: UNIPROT:Q26031; EMBL:L40608; NID:g886374; PID:g886375; PIDN:AAA7539  
C:Genetics:  
A:Gene: var-1  
A:Introns: 2611/3

Query Match 26.7%; Score 54.5; DB 2; Length 3078;  
Best Local Similarity 40.0%; Pred. No. 1.6e+02;  
Matches 12; Conservative 2; Mismatches 15; Indels 1; Gaps 1;

QY 5 YQKCHCHMGTHCHS-SDGPRGVPEPRCP 33  
Db 1698 YPEKCDCYQGHVPSIPPPP?VQFQPEAP 1727

RESULT 11  
A36502  
insulin receptor-related receptor precursor - guinea pig  
C:Species: Cavia porcellus (guinea pig)  
C:Date: 01-Feb-1991 #sequence\_revision 01-Feb-1991 #text\_change 09-Jul-2004  
C:Accession: A36502  
R:Shier, P.; Watt, V.M.  
J. Biol. Chem. 264, 14605-14608, 1989  
A:Title: Primary structure of a putative receptor for a ligand of the insulin family.  
A:Reference number: A36502; MUID:89359245; PMID:2768234  
A:Accession: A36502  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1300 <SHI>  
A:Cross-references: UNIPROT:P14617; GB:J05047  
C:Superfamily: insulin receptor; protein kinase homology  
C:Keywords: ATP; autophosphorylation; phosphoprotein; receptor; transmembrane protein  
F:977-1253/Domain: protein kinase homology <KIN>  
F:985-993/Region: protein kinase ATP-binding motif

Query Match 26.5%; Score 54; DB 2; Length 1300;  
Best Local Similarity 52.6%; Pred. No. 85;  
Matches 10; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

QY 4 YQKCH-CHMGTHCHS 20  
Db 253 YQSACHRACPLGTVEHS 271

RESULT 12  
U1HU  
thyroglobulin precursor, major splice form - human  
C:Species: Homo sapiens (man)  
C:Date: 28-Feb-1986 #sequence\_revision 05-Nov-1999 #text\_change 09-Jul-2004  
C:Accession: A59110; S00014; A01532; S03422; I38343; I57669; S02266; S39432; S66241; S6

R;Malthiery, Y.  
 Submitted to the EMBL Data Library, April 1988  
 A:Description: Human mRNA for thyroglobulin.  
 A:Reference number: A59110  
 A:Accession: A59110  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-2767 <MAL1>  
 A:Cross-references: UNIPROT:P01266; UNIPROT-Q15948; GB:X05615; NID:G37173; PIDN:CAA29104  
 A:Note: revision to S00014  
 R;Malthiery, Y.; Lissitzky, S.  
 Eur. J. Biochem. 165, 491-498, 1987  
 A:Title: Primary structure of human thyroglobulin deduced from the sequence of its 8448-  
 A:Reference number: S00014; MUID:87246630; PMID:3595599  
 A:Accession: S00014  
 A:Molecule type: mRNA  
 A:Residues: 1-1041, 'Y', 1043-1057, 'T', 1059-2767 <MAL2>  
 A:Cross-references: GB:X05615; NID:G37173  
 A:Note: this sequence is revised in A59110  
 R;Malthiery, Y.; Lissitzky, S.  
 Eur. J. Biochem. 147, 53-58, 1985  
 A:Title: Sequence of the 5'-end quarter of the human-thyroglobulin messenger ribonucleic  
 A:Reference number: A01532; MUID:85127024; PMID:3971976  
 A:Accession: A01532  
 A:Molecule type: mRNA  
 A:Residues: 1-730 <MAW>  
 A:Cross-references: GB:X02154; NID:G37175; PIDN:CAA26089.1; PID:G1335349  
 A:Note: the translated sequence in GenBank entry HSTHYRRS, release 111.0, (PIDN:CAA26089  
 n 1-Met  
 R;Parma, J.; Christophe, D.; Pohl, V.; Vassart, G.  
 J. Mol. Biol. 196, 769-779, 1987  
 A:Title: Structural organization of the 5' region of the thyroglobulin gene. Evidence fo  
 A:Reference number: S03422; MUID:88062712; PMID:3681978  
 A:Accession: S03422  
 A:Molecule type: DNA  
 A:Residues: 1-134, 'Q', 136-415, 640-652, 'G', 654-733, 'A', 735-737, 880-983, 'DR', 985-999 <PAR>  
 A:Cross-references: EMBL:X06059; NID:G37145; PIDN:CAA29454.1; PID:G1359884; EMBL:X06067  
 R;Christophe, D.; Cabrer, B.; Bacoll, A.; Targovnik, H.; Pohl, V.; Vassart, G.  
 Nucleic Acids Res. 13, 5129-5144, 1985  
 A:Title: An unusually long poly(purine)-poly(pyrimidine) sequence is located upstream fr  
 A:Reference number: I38343; MUID:85269632; PMID:2991855  
 A:Accession: I38343  
 A:Status: translation not shown; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-22, 'GKX' <CHR>  
 A:Cross-references: EMBL:X02749; NID:G37162; PIDN:CAA26527.1; PID:G759106  
 R;Targovnik, H.M.; Cochaux, P.; Corach, D.; Vassart, G.  
 Mol. Cell. Endocrinol. 84, R23-R26, 1992  
 A:Title: Identification of a minor TG mRNA transcript in RNA from normal and goitrous th  
 A:Reference number: I57669; MUID:93347597; PMID:1639210  
 A:Accession: I57669  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1503-1508, 'L', 1567-1601 <REW>  
 A:Cross-references: GB:S40807; NID:G252170; PIDN:AAB22685.1; PID:G252171  
 A:Note: this sequence fragment represents a minor splice form  
 R;Marrig, C.; Lejeune, P.J.; Venot, N.; Vinet, L.  
 FEBS Lett. 242, 414-418, 1989  
 A:Title: Hormone synthesis in human thyroglobulin: possible cleavage of the polypeptide  
 A:Reference number: S02266; MUID:8912111; PMID:2914619  
 A:Contents: evidence for Tyr-149 as ring donor for thyroxine formation  
 A:Accession: S02266  
 A:Molecule type: protein  
 A:Residues: 101-109, 114-121, 126-131, 143-149 <MAR>  
 A:Note: only the first peptide was sequenced; others were isolated and their amino acid  
 R;Gentile, F.; Salvatore, G.  
 Eur. J. Biochem. 218, 603-621, 1993  
 A:Title: Preferential sites of proteolytic cleavage of bovine, human and rat thyroglobul  
 A:Reference number: S39431; MUID:94094855; PMID:8269951  
 A:Accession: S39431  
 A:Molecule type: protein  
 A:Residues: 20-27, 522-527, 541-547, 616-619, 'X', 621, 1001-1005, 1009-1011, 'X', 1013, 1424-1430  
 R;Xiao, S.; Pollock, H.G.; Targovnik, A.; Rawitch, A.B.  
 Arch. Biochem. Biophys. 320, 96-105, 1995  
 A:Title: Characterization of hormonogenic sites in an N-terminal, cyanogen bromide fragm  
 A:Reference number: S66241; MUID:95314327; PMID:7793989  
 A:Accession: S66241  
 A:Molecule type: protein  
 A:Residues: 'D', 21-23, 45-47, 147-148, 150-152 <XIA>  
 R;Yang, S.X.; Pollock, H.G.; Rawitch, A.B.  
 Arch. Biochem. Biophys. 327, 61-70, 1996  
 A:Title: Glycosylation in human thyroglobulin: location of the N-linked oligosaccharide  
 A:Reference number: S62778; MUID:96201348; PMID:8615697  
 A:Accession: S62778  
 A:Molecule type: protein  
 A:Residues: 69-84, 196-210, 'T', 212-213, 476-492, 523-539, 741-770, 811-848, 850-853, 938-950, 12  
 6-1783, 'D', 1785, 'R', 1999-2017, 2241-2258, 2270-2285, 'P', 2287-2307, 2578-2584 <YAN>  
 R;Ielri, T.; Cochaux, P.; Targovnik, H.M.; Suzuki, M.; Shimoda, S.; Perret, J.; Vassart,  
 J. Clin. Invest. 88, 1901-1905, 1991  
 A:Title: A 3' splice site mutation in the thyroglobulin gene responsible for congenital  
 A:Reference number: I55565; MUID:92091498; PMID:1752952  
 A:Accession: I55565  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 90-91, 160-161 <IEI>  
 A:Cross-references: GB:S71821; NID:G240935; PIDN:AAB20665.1; PID:G240936  
 A:Note: mutant splice form  
 C:Comment: the thyroglobulin molecule is produced in the thyroid gland and is the precur  
 C:Genetics:  
 A:Gene: GDB:TG  
 A:Map position: 8q24.2-8q24.3  
 A:Cross-references: GDB:I20434; OMIM:188450  
 A:Introns: 23/1; 59/2; 92/1; 160/1; 213/2; 249/1; 297/1; 359/1; 726/1; 921/1; 1000/1 #58  
 C:Complex: homodimer  
 C:Function:  
 A:Description: precursor of thyroid hormones thyroxine and triiodothyronine; iodine stor  
 C:Superfamily: thyroglobulin; cholinesterase homology; thyroglobulin type I repeat hcmol  
 C:Keywords: alternative splicing; duplication; glycoprotein; homodimer; iodine; thyroid  
 C:Key-words: signal sequence #status predicted <SIG>  
 F:20-2767/Product: thyroglobulin #status predicted <MAT>  
 F:34-92/Domain: thyroglobulin type I repeat homology <THY1>  
 F:96-160/Domain: thyroglobulin type I repeat homology <THY2>  
 F:164-297/Domain: thyroglobulin type I repeat homology #status atypical <THY3>  
 F:301-358/Domain: thyroglobulin type I repeat homology <THY4>  
 F:608-658/Domain: thyroglobulin type I repeat homology <THY5>  
 F:662-726/Domain: thyroglobulin type I repeat homology <THY6>  
 F:730-921/Domain: thyroglobulin type I repeat homology #status atypical <THY7>  
 F:925-1072/Domain: thyroglobulin type I repeat homology #status atypical <THY8>  
 F:1076-1144/Domain: thyroglobulin type I repeat homology <THY9>  
 F:1148-1209/Domain: thyroglobulin type I repeat homology <TH10>  
 F:1455-1468/Region: type II repeat  
 F:1469-1485/Region: type II repeat  
 F:1486-1502/Region: type II repeat  
 F:1602-1722/Region: type IIIa repeat  
 F:1723-1891/Region: type IIIb repeat  
 F:1892-1994/Region: type IIIa repeat  
 F:1995-2128/Region: type IIIb repeat  
 F:2129-2186/Region: type IIIa repeat  
 F:2227-2725/Domain: cholinesterase homology <ACE>  
 F:224, 2572, 2586/Modified site: thyroxine (Tyr) #status predicted  
 F:76, 198, 484, 529, 748, 816, 947, 1219, 1348, 1364, 1715, 1773, 2012, 2249, 2294, 2581/Binding site:  
 F:110, 496, 1868, 2121/Binding site: carbohydrate (Asn) (covalent) #status absent  
 F:149/Modified site: dehydroalanine (Tyr) #status predicted  
 F:2765/Modified site: triiodothyronine (Tyr) #status predicted  
 Query Match 26.2%; Score 53.5; DB 1; Length 2767;  
 Best Local Similarity 31.2%; Pred. No. 1.9e+02;  
 Matches 15; Conservative 2; Mismatches 12; Indels 19; Gaps 3;  
 QY 5 YQKGC-----HCNMG-T-HCHSSDGRGVPE-----PRCP 33  
 DB 1026 YMFQCDAFGSWEPEVQCHAGTGHCMVDEKGFIPGSLTARSLQIPQCP 1073  
 RESULT 13  
 D37679

argininosuccinate synthase (PA3525) [imported] - Agrobacterium tumefaciens (strain C59,  
C:Species: Agrobacterium tumefaciens  
C:Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 18-Nov-2002  
C:Accession: D97679  
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorllo, B.; Goldman,  
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markels, B.;  
Science 294, 2323-2328, 2001  
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum  
A:Reference number: A97359; MUID:21608551; PMID:11743194  
A:Accession: D97679  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-460 <KUR>  
A:Cross-references: GB:AB007869; PIDN:AAK88389.1; PID:G15157878; GSPDB:GN00169  
C:Genetics:  
A:Gene: AGR C 4836  
A:Map position: circular chromosome  
C:Superfamily: argininosuccinate synthase

Query Match 26.0%; Score 53; DB 2; Length 460;  
Best Local Similarity 40.0%; Pred. No. 44;  
Matches 12; Conservative 3; Mismatches 11; Indels 4; Gaps 1;  
QY 4 YQGGKCHCHMGTHCHSSDGRGVIPERCP 33  
DB 18 YLTKRTRTHGLCKSAEIPR----KWRCP 43

RESULT 14  
T16006  
Protein kinase C3 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: T16006; T37253  
R:Chisoe, S.  
submitted to the EMBL Data Library, September 1995  
A:Description: The sequence of C. elegans cosmid F09E5.  
A:Reference number: Z1844  
A:Accession: T16006  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-597 <CHI>  
A:Cross-references: UNIPROT:Q19266; EMBL:U37429; NID:G1019949; PID:G1019950; PIDN:AAA793  
A:Experimental source: strain Bristol N2  
R:Wu, S.L.; Rubin, C.S.  
submitted to the EMBL Data Library, September 1997  
A:Description: Molecular characterization of an atypical protein kinase C from C. elegans  
A:Reference number: Z21647  
A:Accession: T37253  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-597 <WUS>  
A:Cross-references: EMBL:AF025666; PIDN:AAB88885.1  
A:Experimental source: strain Bristol N2  
C:Genetics:  
A:Gene: F09E5.1; pkc-3  
A:Map position: II  
A:Introns: 22/3; 109/1; 137/2; 179/3; 238/3; 322/3; 442/2; 556/3  
C:Superfamily: protein kinase C, zeta/iota type; protein kinase C zinc-binding repeat hc  
F:128-177/Domain: protein kinase C zinc-binding repeat homology <KZN>  
F:251-522/Domain: protein kinase homology <KIN>

Query Match 26.0%; Score 53; DB 2; Length 597;  
Best Local Similarity 50.0%; Pred. No. 56;  
Matches 11; Conservative 3; Mismatches 6; Indels 2; Gaps 2;  
QY 8 KCHCHMGTHC-HSSDGRGVIP 28  
DB 168 KCHRVTRTHCGQALQGP-NIIP 188

RESULT 15  
S37486

gene msg3 protein - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
C:Accession: I48671; S37486  
R:Tronik-Le Roux, D.; Senorale-Pose, M.; Rougeon, F.  
Gene 142, 175-182, 1994  
A:Title: Three novel SMR1-related cDNAs characterized in the submaxillary gland of mice  
A:Reference number: I48669; MUID:94252564; PMID:8194749  
A:Accession: I48671  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-91 <RES>  
A:Cross-references: UNIPROT:Q61902; EMBL:X71631; NID:G406260; PIDN:CAAS0638.1; PID:G406  
C:Genetics:  
A:Gene: msg3  
C:Superfamily: proline-rich peptide P-B

Query Match 25.7%; Score 52.5; DB 2; Length 91;  
Best Local Similarity 45.5%; Pred. No. 12;  
Matches 10; Conservative 0; Mismatches 9; Indels 3; Gaps 1;  
QY 9 CHCHMGTHCHSSDGRGVIP 30  
DB 20 CECHRGPRRD--PRGFFPPP 38

Search completed: November 16, 2004, 19:15:56  
Job time : 8.82759 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 16, 2004, 18:56:15 ; Search time 36.8515 seconds  
(without alignments)  
515.240 Million cell updates/sec

Title: US-10-036-444-6

Perfect score: 204

Sequence: 1 STVYQKCHCHMGTHCHSDSGRGPVPEPRCP 33

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_02.4

1: uniprot\_sprot.4

2: uniprot\_trembl.4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	142	69.6	180	1 NCT3_MACMU	Q8mj02 macaca mula
2	119	58.3	176	1 NCT3_MACFA	P61483 macaca fasc
3	67	32.8	192	1 NCT3_RAT	Q8cf09 rattus norv
4	63.5	31.1	665	2 Q7VZW9	Q7vzw9 bordetella
5	63.5	31.1	665	2 Q7WLN6	Q7wln6 bordetella
6	63.5	31.1	665	2 Q7WQ11	Q7wq11 bordetella
7	61	29.9	485	2 Q97271	Q97271 plasmodium
8	60	29.4	201	1 NCT3_HUMAN	O14931 homo sapien
9	60	29.4	201	1 NCT3_PANTR	P61484 pan troglod
10	60	29.4	371	2 Q7RC43	Q7rc43 plasmodium
11	60	29.4	1799	1 LMB2_MOUSE	Q61292 mus musculu
12	60	29.4	1799	2 Q8R0Y0	Q8r0y0 mus musculu
13	60	29.4	1801	1 LMB2_RAT	P15800 rattus norv
14	59.5	29.2	660	1 VHL1_EBV	P03181 epstein-bar
15	59.5	29.2	660	2 Q777A3	Q777a3 human herpe
16	59.5	29.2	660	2 CAD53473	Cad53473 human her
17	59.5	29.2	3170	2 Q7FNS0	Q7fn80 anopheles g
18	59	28.9	544	2 Q9X822	Q9x822 streptomyce
19	58.5	28.7	116	2 Q9NT74	Q9nt74 homo sapien
20	58.5	28.7	2471	1 NCT2_HUMAN	Q04721 homo sapien
21	58	28.4	180	2 Q82257	Q82257 arabidopsis
22	58	28.4	845	1 AD09_MOUSE	Q61072 mus musculu
23	57.5	28.2	198	2 Q89070	Q89070 human herpe
24	57.5	28.2	881	2 Q9W0A0	Q9w0a0 drosophila
25	56.5	27.7	969	2 Q96K96	Q96k96 homo sapien
26	56.5	27.7	1140	2 Q80T91	Q80t91 mus musculu
27	56	27.5	131	2 Q6IK23	Q6ik23 drosophila
28	55.5	27.2	117	2 Q6SWP9	Q6swp9 human cytom
29	55.5	27.2	117	2 AAR31547	Aar31547 human cyt
30	55.5	27.2	1140	2 Q96KG7	Q96kg7 homo sapien
31	55.5	27.2	1147	2 Q6DIB5	Q6dib5 mus musculu

32 55.5 27.2 2931 2 Q9W2C6 Q9w2c6 drosophila  
33 55.5 27.2 2968 2 Q8MLU9 Q8mlu9 drosophila  
34 55.5 27.2 2968 2 AAW71018 Aaw71018 drosophila  
35 55 27.0 178 2 Q6P750 Q6p750 rattus norv  
36 55 27.0 178 2 AAH61833 Aah61833 rattus norv  
37 55 27.0 299 2 Q6GQ38 Q6gq38 xenopus lae  
38 55 27.0 744 2 Q7Q7D9 Q7q7d9 anopheles g  
39 55 27.0 1664 2 Q8TVQ2 Q8tvq2 caenorhabdi  
40 54.5 26.7 144 2 Q8DJ62 Q8dj62 synchococc  
41 54.5 26.7 147 1 SMX1\_MOUSE SMx1 mouse  
42 54.5 26.7 680 2 Q6MYU6 Q6myu6 aspergillus  
43 54.5 26.7 680 2 CAE47913 Cae47913 aspergill  
44 54.5 26.7 814 2 Q6ZWJ8 Q6zwj8 homo sapien  
45 54.5 26.7 814 2 BAC85504 Bac85504 homo sapi

#### ALIGNMENTS

##### RESULT 1

NCT3\_MACMU  
ID NCT3\_MACMU STANDARD; PRT; 180 AA.  
AC Q8MJ02; Q8MJ00; Q8MJ01; Q95JB8;  
DT 05-JUL-2004 (Rel. 44, Created)  
DT 05-JUL-2004 (Rel. 44, Last sequence update)  
DT 01-OCT-2004 (Rel. 45, Last annotation update)  
DE Natural cytotoxicity triggering receptor 3 precursor (Natural killer  
DE cell p30-related protein) (NKP30) (NK-p30).  
GS Name=NCR3;  
OS Macaca mulatta (Rhesus macaque).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;  
OC Cercopitheciinae; Macaca.  
OX NCBI\_TaxID=9544;  
[1]  
RN SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4), AND VARIANT VAL-156.  
RP LaBonte M.L., Miller J., Letvin N.L.;  
RA "Molecular cloning of rhesus monkey NKP46 and NKP30 and identification  
RT of NKP46SD and NKP30S.";  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBSJ databases.  
[2]  
RN SEQUENCE FROM N.A. (ISOFORMS 1 AND 4), AND VARIANT VAL-156.  
RP TISSUE=Lymphoid;  
RC Rizzi M., Biassoni R.;  
RA "NCR expressed by macaca NK cells.";  
RT Submitted (MAR-2003) to the EMBL/GenBank/DBSJ databases.  
RL -!- FUNCTION: Cytotoxicity activating receptor that may contribute to  
CC the increased efficiency of activated natural killer (NK) cells to  
CC mediate tumor cell lysis (By similarity).  
CC -!- SUBUNIT: Interacts with CD32 (By similarity).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=4;  
CC Name=1;  
CC IsoId=Q8MJ02-1; Sequence=Displayed;  
CC Note=No experimental confirmation available;  
CC Name=2;  
CC IsoId=Q8MJ02-2; Sequence=VSP\_010414;  
CC Note=No experimental confirmation available;  
CC Name=3;  
CC IsoId=Q8MJ02-3; Sequence=VSP\_010415, VSP\_010416;  
CC Note=No experimental confirmation available;  
CC Name=4;  
CC IsoId=Q8MJ02-4; Sequence=VSP\_010417;  
CC Note=No experimental confirmation available;  
CC -!- SIMILARITY: Belongs to natural cytotoxicity receptor (NCR) family.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
-----  
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CC -----
CC EMBL; AY035214; AAKG31116.1; -
CC EMBL; AY035215; AAKG31117.1; -
CC EMBL; AY035216; AAKG31118.1; -
CC EMBL; AY035217; AAKG31119.1; -
CC EMBL; AJ554301; CAD86942.1; -
CC HSSP; P16410; 1185.
CC InterPro; IPR003599; IG.
CC InterPro; IPR007110; IG-like.
CC SMART; SM00409; IG; 1.
CC PROSITE; PS50835; IG LIKE; 1.
KW Alternative splicing; Glycoprotein; Immunoglobulin domain;
KW Polymorphism; Receptor; Signal; Transmembrane.
FT SIGNAL 1 18
FT CHAIN 19 180
FT Natural cytotoxicity triggering receptor
FT DOMAIN 19 133
FT TRANSMEM 134 154
FT DOMAIN 155 180
FT DOMAIN 159 126
FT DISULFID 39 108
FT CARBOHYD 42 42
FT CARBOHYD 121 121
FT VARSPLIC 66 90
FT VARSPLIC 112 115
FT VARSPLIC 116 180
FT VARSPLIC 177 180
FT VARIANT 156 156
FT SEQUENCE 180 AA; 19639 MW; 5C2DF53487B2A3B6 CRC64;
Query Match 69.6%; Score 142; DB 1; Length 180;
Best Local Similarity 95.7%; Pred. No. 4.8e-10;
Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STVYQKCHCHMGTHCHSSDGP 23
Db 158 STLYYQKCHCHMGTHCHSSDGP 180

RESULT 2
NCT3 MACFA STANDARD; PRT; 176 AA.
AC P61483; Q95JB8;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Natural cytotoxicity triggering receptor 3 precursor (Natural killer
DE cell p30-related protein) (NKP30) (NK-p30).
GN Name=NCR3; Synonyms=IC7;
OS Rattus norvegicus (Rat);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphoid;
RA Rizzi M., Biassoni R.;
RT Macaca fascicularis lymphoid cells.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Cytotoxicity activating receptor that may contribute to
CC the increased efficiency of activated natural killer (NK) cells to
CC mediate tumor cell lysis (By similarity).
CC -!- SUBUNIT: Interacts with CD32 (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -----
CC -----
CC -!- SIMILARITY: Belongs to natural cytotoxicity receptor (NCR) family.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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DR	EWBL; BX883046; CAE84000.1; -	
DR	HSSP; P09793; IDQT.	
DR	RGD; 727881; 1C7.	
DR	InterPro; IPR003599; Ig.	
DR	InterPro; IPR007110; Ig-like.	
DR	Pfam; PF00047; Ig; 1.	
DR	SMART; SM00409; Ig; 1.	
DR	PROSITE; PS50835; IG LIKE; 1.	
DR	Glycoprotein; immunoglobulin domain; Polymorphism; Receptor; Signal;	
KW	Transmembrane.	
FT	SIGNAL	1 18
FT	CHAIN	19 192
FT		Potential.
FT		Natural cytotoxicity triggering receptor
FT		3.
FT	DOMAIN	19 147 Extracellular (Potential).
FT	TRANSXEM	148 168 Potential.
FT	DOMAIN	169 192 Cytoplasmic (Potential).
FT	DOMAIN	19 126 Ig-like.
FT	DISULFID	39 108 By similarity.
FT	VARIANT	7 7 I -> V.
FT	VARIANT	19 19 I -> V.
FT	VARIANT	82 82 A -> V.
FT	VARIANT	138 138 A -> T.
FT	CONFLICT	135 135 A -> V (in Ref. 2).
FT	SEQUENCE	192 AA; 20470 MW; 7FC94FB25D22377 CRC64;
QY	Query Match	32.8%; Score 67; DB 1; Length 192;
DB	Best Local Similarity	71.4%; Pred. No. 1.5;
	Matches 10; Conservative	2; Mismatches 2; Indels 0; Gaps 0;
QY	1 STVYVGKCHCHMG 14	
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DB	166 SVIYVGKCLCHVG 179	
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ID	Q7VZW9 PRELIMINARY; PRT; 665 AA.	
AC	Q7VZW9;	
DT	01-OCT-2003 (TrEMBLrel. 25, Created)	
DT	01-OCT-2003 (TrEMBLrel. 25, Last sequence update)	
DE	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)	
DE	Hydantoin utilization protein B.	
GN	Nameshub; OrderedlocusNames=BP0754;	
CS	Bordetella pertussis.	
OC	Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;	
OC	Alcaligenaceae; Bordetella.	
OC	NCBI_TaxID=520;	
RP	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=Tohana I / ATCC BAA-589 / NCTC 13251;	
RX	MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;	
RA	Parkhill J., Sebathia M., Preston A., Murphy L.D., Thomson N.R.,	
RA	Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,	
RA	Cardeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,	
RA	Achtman M., Atkin R., Baker S., Basham A., Bason N., Cherevach I.,	
RA	Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,	
RA	Feltwell T., Goble A., Hamlin N., Hauser H., Holtroyd S., Jagels K.,	
RA	Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,	
RA	Rabinowitz E., Rutter S., Sanders M., Saunders D., Seeger K.,	
RA	Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,	
RA	Unwin L., Whitehead S., Barrrell B.G., Maskell D.J.;	
RT	"Comparative analysis of the genome sequences of Bordetella pertussis,	
RT	Bordetella parapertussis and Bordetella bronchiseptica.";	
RL	Nat. Genet. 35:32-40(2003).	
DR	EWBL; BX640413; CAE41060.1; -	
DR	GO; GO:0003824; F:catalytic activity; IEA.	
DR	InterPro; IPR005479; Cphp synth_L_D2.	
DR	InterPro; IPR003692; Hydantoinase B.	
DR	Pfam; PF02538; Hydantoinase B; 1.	
DR	PROSITE; PS00867; CFSASE_2; UNKNOWN_1.	
KW	Complete Proteome.	
QO	SEQUENCE 665 AA; 72395 MW; F27204349A190508 CRC64;	

Query Match 31.1%; Score 63.5; DB 2; Length 665;  
 Best Local Similarity 46.2%; Pred. No. 14;  
 Matches 12; Conservative 5; Mismatches 8; Indels 1; Gaps 1;

Qy 3 VYQKGCHCHMGTHCHSSDGRGVIP 28

Db 108 VYQGMVCFVGGHINTD-MGGAVP 132

RESULT 5

Q7W1N6 PRELIMINARY; PRT; 665 AA.  
 AC Q7W1N6;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Hydanotoin utilization protein B.  
 GN Name=HyuB; OrderedLocusNames=BPP0316;  
 OS Bordetella parapertussis.  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
 OC Alcaligenaceae; Bordetella.  
 OX NCBI\_TaxID=519;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=12822 / ATCC BAA-587;  
 RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;  
 RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.R.,  
 RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,  
 RA Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,  
 RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,  
 RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,  
 RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,  
 RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,  
 RA Rabinowitsch E., Rutter S., Saunders M., Saunders D., Seeger K.,  
 RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,  
 RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;  
 RT "Comparative analysis of the genome sequences of Bordetella pertussis,  
 RT Bordetella parapertussis and Bordetella bronchiseptica.";  
 RL Nat. Genet. 35:32-40(2003).  
 DR EMBL; BX640423; CAE40057.1;  
 DR GO; GO:0003824; F:catalytic activity; IEA.  
 DR InterPro; IPR005479; Cphp synth\_L D2.  
 DR Pfam; PF02538; Hydanotoinase\_B.  
 DR Prosite; PS00867; Hydanotoinase\_B; 1.  
 DR Complete proteome.  
 KW NCBI\_TaxID=519;  
 SQ SEQUENCE 665 AA; 72497 MW; 5B2BEFC6DDE39D2 CRC64;  
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Query Match 31.1%; Score 63.5; DB 2; Length 665;  
 Best Local Similarity 46.2%; Pred. No. 14;  
 Matches 12; Conservative 5; Mismatches 8; Indels 1; Gaps 1;

Qy 3 VYQKGCHCHMGTHCHSSDGRGVIP 28

Db 108 VYQGMVCFVGGHINTD-MGGAVP 132

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Q7WQ11 PRELIMINARY; PRT; 665 AA.  
 AC Q7WQ11;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Hydanotoin utilization protein B.  
 GN Name=hyuB; OrderedLocusNames=BB0319;  
 OS Bordetella bronchiseptica (Alcaligenes bronchisepticus).  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
 OC Alcaligenaceae; Bordetella.  
 OX NCBI\_TaxID=518;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=RB50 / ATCC BAA-588;  
 RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;  
 RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.R.,  
 RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,  
 RA Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,  
 RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,  
 RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,  
 RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,  
 RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,  
 RA Rabinowitsch E., Rutter S., Saunders M., Saunders D., Seeger K.,  
 RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,  
 RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;  
 RT "Comparative analysis of the genome sequences of Bordetella pertussis,  
 RT Bordetella parapertussis and Bordetella bronchiseptica.";  
 RL Nat. Genet. 35:32-40(2003).  
 DR EMBL; BX640423; CAE40057.1;  
 DR GO; GO:0003824; F:catalytic activity; IEA.  
 DR InterPro; IPR005479; Cphp synth\_L D2.  
 DR Pfam; PF02538; Hydanotoinase\_B; 1.  
 DR Prosite; PS00867; Hydanotoinase\_B; 1.  
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RESULT 7

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 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Hypothetical protein MAL3P5.20.  
 GN Name=MAL3P5.20; Synonyms=PF0680W;  
 OS Plasmodium falciparum (isolate 3D7).  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 OX NCBI\_TaxID=36329;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99376085; PubMed=10448855;  
 RA Bowman S., Lawson D., Basham D., Brown D., Chillingworth T.,  
 RA Churcher C.M., Craig A., Davies R.M., Devlin K., Feltwell T.,  
 RA Gentles S., Gwilliam R., Hamlin N., Harris D., Holroyd S., Hornsby T.,  
 RA Horrocks P., Jagels K., Jassal B., Kyes S., Mclean J., Moule S.,  
 RA Mungall K., Murphy L., Oliver K., Quail M.A., Rajandream M.-A.,  
 RA Rutter S., Skelton J., Squares R., Squares S., Sulston J.E.,  
 RA Whitehead S., Woodward J.R., Newbold C., Barrell B.G.;  
 RT "The complete nucleotide sequence of chromosome 3 of Plasmodium  
 RT falciparum.";  
 RL Nature 400:532-538 (1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22255708; PubMed=12368867;  
 RA Hall N., Pain A., Berriman M., Churcher C., Harris B., Harris D.,  
 RA Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,  
 RA Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,  
 RA Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,  
 RA Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,  
 RA Feltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,  
 RA Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,  
 RA Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,  
 RA Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,  
 RA Line A., Maddison M., Mclean J., Mooney P., Moule S., Murphy L.,  
 RA Oliver K., Ormond D., Price C., Quail M.A., Rabinowitsch E.,  
 RA Rajandream M.-A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,  
 RA Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,

Query Match 31.1%; Score 63.5; DB 2; Length 665;  
 Best Local Similarity 46.2%; Pred. No. 14;  
 Matches 12; Conservative 5; Mismatches 8; Indels 1; Gaps 1;

Qy 3 VYQKGCHCHMGTHCHSSDGRGVIP 28

Db 108 VYQGMVCFVGGHINTD-MGGAVP 132

RESULT 7

Q7W271 PRELIMINARY; PRT; 485 AA.  
 AC Q7W271;  
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Hypothetical protein MAL3P5.20.  
 GN Name=MAL3P5.20; Synonyms=PF0680W;  
 OS Plasmodium falciparum (isolate 3D7).  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 OX NCBI\_TaxID=36329;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99376085; PubMed=10448855;  
 RA Bowman S., Lawson D., Basham D., Brown D., Chillingworth T.,  
 RA Churcher C.M., Craig A., Davies R.M., Devlin K., Feltwell T.,  
 RA Gentles S., Gwilliam R., Hamlin N., Harris D., Holroyd S., Hornsby T.,  
 RA Horrocks P., Jagels K., Jassal B., Kyes S., Mclean J., Moule S.,  
 RA Mungall K., Murphy L., Oliver K., Quail M.A., Rajandream M.-A.,  
 RA Rutter S., Skelton J., Squares R., Squares S., Sulston J.E.,  
 RA Whitehead S., Woodward J.R., Newbold C., Barrell B.G.;  
 RT "The complete nucleotide sequence of chromosome 3 of Plasmodium  
 RT falciparum.";  
 RL Nature 400:532-538 (1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22255708; PubMed=12368867;  
 RA Hall N., Pain A., Berriman M., Churcher C., Harris B., Harris D.,  
 RA Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,  
 RA Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,  
 RA Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,  
 RA Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,  
 RA Feltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,  
 RA Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,  
 RA Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,  
 RA Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,  
 RA Line A., Maddison M., Mclean J., Mooney P., Moule S., Murphy L.,  
 RA Oliver K., Ormond D., Price C., Quail M.A., Rabinowitsch E.,  
 RA Rajandream M.-A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,  
 RA Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,

RA Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,  
RA Sulston J.E., Craig A., Newbold C., Barrell B.G;  
RT "Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13."  
RL Nature 419:527-531(2002).  
DR EMBL; AL034556; CAB38982.3; --  
DR InterPro; IPR000345; CytC\_heme\_BS.  
DR PROSITE; PS00190; CYTOCHROME\_C; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 485 AA; 57072 MW; 59C4467FC026C472 CRC64;  
Query Match 29.9%; Score 61; DB 2; Length 485;  
Best Local Similarity 25.0%; Pred. No. 21;  
Matches 11; Conservative 10; Mismatches 7; Indels 16; Gaps 2;  
Qy 4 YQCKKCH-----CHMGTHC-----HSDGGRGVIPPEPR 31  
Db 156 HHKGRCSFKYEWYTRGCHLGRFCFHCDQSHVPEGRVVPNQ 199  
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NCT3\_HUMAN STANDARD; PRT; 201 AA.  
AC O14931; O14930; O14932; O95667; O95668; O95669;  
DT 05-JUL-2004 (Rel. 44, Created)  
DT 05-JUL-2004 (Rel. 44, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Natural cytotoxicity triggering receptor 3 precursor (Natural killer  
DE cell p30-related protein) (NKP30) (NK-p30).  
GN Name=NCR3; Synonyms=IC7;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
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RP CD3Z, AND FUNCTION.  
RC TISSUE=Lymphoid;  
RX PubMed=10562324;  
RA Pende D., Parolini S., Pessino A., Sivori S., Augugliaro R.,  
RA Morelli L., Marcenaro E., Accame L., Malaespina A., Biasoni R.,  
RA Bottino C., Moretta L., Moretta A.;  
RT "Identification and molecular characterization of NKP30, a novel  
RT triggering receptor involved in natural cytotoxicity mediated by human  
RT natural killer cells."  
RL J. Exp. Med. 190:1505-1516(1999).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM 2), TISSUE SPECIFICITY, AND INTERACTION  
RP WITH CD3Z.  
RC TISSUE=peripheral blood;  
RX Sato M., Yabe T., Ohashi J., Tsuchiya N., Hanaoka K., Tokura K.,  
RA Fuji T.;  
RT "Identification of two novel single nucleotide polymorphisms in the  
RT NKP30 gene in human natural killer cells."  
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4; 5 AND 6).  
RX MEDLINE=99218514; PubMed=10202016;  
RA Neville M.J., Campbell R.D.;  
RT "A new member of the Ig superfamily and a V-ATPase G subunit are among  
RT the predicted products of novel genes close to the TNF locus in the  
RT human MHC."  
RL J. Immunol. 162:4745-4754(1999).  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
RC TISSUE=spleen;  
RX MEDLINE=96422187; PubMed=8824804;  
RA Nalabolu S.R., Shukla H., Nallur G., Parimoo S., Weissman S.M.;  
RT "Genes in a 220-kb region spanning the TNF cluster in human MHC."  
RL Genomics 31:215-222(1996).  
RN [5]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RX PubMed=1465967; DOI=10.1101/gr.1736803;  
RA Xie T., Rowen L., Aguado B., Ahearn M.E., Madan A., Qin S.,

RA Campbell R.D., Hood L.;  
RT "Analysis of the gene-dense major histocompatibility complex class III  
RT region and its comparison to mouse."  
RL Genome Res. 13:2621-2636(2003).  
RN [6]  
RP SEQUENCE FROM N.A. (ISOFORM 3).  
RA Shiina S., Tamiya G., Oka A., Inoko H.;  
RT "Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region."  
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
RN [7]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC TISSUE=Blood;  
RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -!- FUNCTION: Cytotoxicity activating receptor that may contribute to  
CC the increased efficiency of activated natural killer (NK) cells to  
CC mediate tumor cell lysis.  
CC -!- SUBUNIT: Interacts with CD3Z.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=6;  
CC Name=1; Synonyms=IC7a;  
CC IsoId=O14931-1; Sequence=Displayed;  
CC Note=No experimental confirmation available;  
CC Name=2; Synonyms=IC7c;  
CC IsoId=O14931-2; Sequence=VSP\_010413;  
CC Note=No experimental confirmation available;  
CC Name=3; Synonyms=IC7b;  
CC IsoId=O14931-3; Sequence=VSP\_010412;  
CC Note=No experimental confirmation available;  
CC Name=4; Synonyms=IC7e;  
CC IsoId=O14931-4; Sequence=VSP\_010411;  
CC Note=No experimental confirmation available;  
CC Name=5; Synonyms=IC7f;  
CC IsoId=O14931-5; Sequence=VSP\_010411, VSP\_010413;  
CC Note=No experimental confirmation available;  
CC Name=6; Synonyms=IC7d;  
CC IsoId=O14931-6; Sequence=VSP\_010411, VSP\_010412;  
CC Note=No experimental confirmation available;  
CC -!- TISSUE SPECIFICITY: Selectively expressed by all resting and  
CC activated NK cells and weakly expressed in spleen.  
CC -!- SIMILARITY: Belongs to natural cytotoxicity receptor (NCR) family.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
CC -----  
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CC or send an email to license@sib-sib.ch).  
CC -----  
CC EMBL; AJ223153; CAB54004.1; --  
CC EMBL; AB055881; BAB78472.1; --



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DR InterPro: IPR000345; CytC_heme_BS.
DR PROSITE: PS00190; CYTOCHROME_C; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 371 AA; 43542 MW; BC325F6C5B8D8B36 CRC64;
Query Match 29.4%; Score 60; DB 2; Length 371;
Best Local Similarity 35.7%; Pred. No. 22;
Matches 15; Conservative 5; Mismatches 6; Indels 16; Gaps 3;
QY 6 QGKCH-----CHNGTHC-----HSDGPRG-----VIEPR 31
DB 145 KGTCNFCVYEWTRGCHMGKFCRCHHSHVPIGTARVWDPK 186
RESULT 11
LMB2_MOUSE
ID LMB2_MOUSE STANDARD; PRT; 1799 AA.
AC Q61232; Q62182;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Laminin beta-2 chain precursor (S-laminin) (S-LAM).
GN Names=Lamb2; Synonyms=Lams;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/J;
RX MEDLINE=96278760; PubMed=8662701;
RA Durkin M.E., Gautam M., Loechel S., Sanes J.R., Merlie J.P.,
RA Albrechtsen R., Wewer U.M.;
RT "Structural organization of the human and mouse laminin beta2 chain
RT genes, and alternative splicing at the 5' end of the human
RT transcript.";
RL J. Biol. Chem. 271:13407-13416(1996).
RN [2]
RP SEQUENCE OF 348-428 FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=94319092; PubMed=8043959;
RA Aberdam D., Galliano M.F., Mattai M.-G., Ortonne J.P., Meneguzzi G.;
RT "S-laminin gene (Lams) maps to F1 band of mouse chromosome 9.";
RL Mamm. Genome 5:393-394(1994).
RN [3]
RP FUNCTION.
RC STRAIN=129/J;
RX MEDLINE=95191650; PubMed=7885444;
RA Neakes P.G., Gautam M., Mudd J., Sanes J.R., Merlie J.P.;
RT "Aberrant differentiation of neuromuscular junctions in mice lacking
RT S-laminin/laminin beta 2.";
RL Nature 374:258-262(1995).
CC -|- FUNCTION: Binding to cells via a high affinity receptor, laminin
CC is thought to mediate the attachment, migration and organization
CC of cells into tissues during embryonic development by interacting
CC with other extracellular matrix components.
CC -|- FUNCTION: Laminin-3 (S-laminin) regulates the formation of motor
CC nerve terminals.
CC -|- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
CC different polypeptide chains (alpha, beta, gamma), which are bound
CC to each other by disulfide bonds into a cross-shaped molecule
CC comprising one long and three short arms with globules at each
CC end. The beta-2 chain is a subunit of laminin-3 (S-laminin),
CC laminin-4 (S-merosin), and laminin-7 (KS-laminin).
CC -|- SUBCELLULAR LOCATION: Extracellular; found in the basement
CC membranes (major component).
CC -|- TISSUE SPECIFICITY: Neuromuscular synapse and kidney glomerulus.
CC -|- DOMAIN: The alpha-helical domains I and II are thought to interact
CC with other laminin chains to form a coiled coil structure.
CC -|- DOMAIN: Domains VI and IV are globular.
CC -|- SIMILARITY: Contains 13 laminin EGF-like domains.
CC -|- SIMILARITY: Contains 1 laminin IV domain.
CC -|- SIMILARITY: Contains 1 laminin N-terminal domain.

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EMBL; U43541; AAC53535.1; -  
EMBL; U42624; AAC53535.1; JOINED.  
EMBL; X75928; CAA53532.1; -  
HSSP; P02468; 1NPE.  
MGI; MGI:99916; Lamb2.  
InterPro; IPR006209; EGF like.  
InterPro; IPR008979; Gal\_bind\_like.  
InterPro; IPR002049; Laminin\_EGF.  
InterPro; IPR008211; Laminin\_N.  
Pfam; PF00053; Laminin\_EGF; 12.  
Pfam; PF00055; Laminin\_N; 1.  
PRINTS; PS00011; EGF\_LAMININ.  
PROSITE; PS00022; EGF\_1; 10.  
PROSITE; PS01186; EGF\_2; 2.  
PROSITE; PS01248; LAMININ\_TYPE\_EGF; 12.  
Basement membrane; Cell adhesion; Coiled coil; Extracellular matrix;  
KW Glycoprotein; Laminin EGF-like domain; Repeat; Signal.  
FT SIGNAL 1 35 Potential.  
FT CHAIN 36 1799 Laminin beta-2 chain.  
FT DOMAIN 36 283 Laminin N-terminal (domain VI).  
FT DOMAIN 286 349 Laminin EGF-like 1.  
FT DOMAIN 350 412 Laminin EGF-like 2.  
FT DOMAIN 413 472 Laminin EGF-like 3.  
FT DOMAIN 473 524 Laminin EGF-like 4.  
FT DOMAIN 525 555 Laminin EGF-like 5 (incomplete).  
FT DOMAIN 556 782 Laminin domain IV.  
FT DOMAIN 784 831 Laminin EGF-like 6.  
FT DOMAIN 832 877 Laminin EGF-like 7.  
FT DOMAIN 878 927 Laminin EGF-like 8.  
FT DOMAIN 928 986 Laminin EGF-like 9.  
FT DOMAIN 987 1038 Laminin EGF-like 10.  
FT DOMAIN 1039 1095 Laminin EGF-like 11.  
FT DOMAIN 1096 1143 Laminin EGF-like 12.  
FT DOMAIN 1144 1190 Laminin EGF-like 13.  
FT DOMAIN 1191 1410 Domain II.  
FT DOMAIN 1411 1443 Domain alpha.  
FT DOMAIN 1444 1799 Domain I.  
FT DOMAIN 1257 1304 Coiled coil (Potential).  
FT DOMAIN 1473 1527 Coiled coil (Potential).  
FT DOMAIN 1577 1791 Coiled coil (Potential).  
FT DISULFID 286 295 By similarity.  
FT DISULFID 288 313 By similarity.  
FT DISULFID 315 324 By similarity.  
FT DISULFID 327 347 By similarity.  
FT DISULFID 350 359 By similarity.  
FT DISULFID 352 377 By similarity.  
FT DISULFID 380 389 By similarity.  
FT DISULFID 392 410 By similarity.  
FT DISULFID 413 426 By similarity.  
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FT DISULFID 473 487 By similarity.  
FT DISULFID 475 494 By similarity.  
FT DISULFID 496 505 By similarity.  
FT DISULFID 508 522 By similarity.  
FT DISULFID 784 796 By similarity.  
FT DISULFID 786 803 By similarity.  
FT DISULFID 805 814 By similarity.  
FT DISULFID 817 829 By similarity.  
FT DISULFID 832 844 By similarity.  
FT DISULFID 834 851 By similarity.  
FT DISULFID 853 862 By similarity.  
FT DISULFID 865 875 By similarity.



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FT DISULFID 878 887 By similarity.
FT DISULFID 880 894 By similarity.
FT DISULFID 897 906 By similarity.
FT DISULFID 909 925 By similarity.
FT DISULFID 928 944 By similarity.
FT DISULFID 930 955 By similarity.
FT DISULFID 957 966 By similarity.
FT DISULFID 969 984 By similarity.
FT DISULFID 987 1001 By similarity.
FT DISULFID 989 1008 By similarity.
FT DISULFID 1011 1020 By similarity.
FT DISULFID 1023 1036 By similarity.
FT DISULFID 1036 1108 By similarity.
FT DISULFID 1098 1115 By similarity.
FT DISULFID 1117 1126 By similarity.
FT DISULFID 1129 1141 By similarity.
FT DISULFID 1144 1156 By similarity.
FT DISULFID 1146 1163 By similarity.
FT DISULFID 1165 1174 By similarity.
FT DISULFID 1177 1188 By similarity.
FT DISULFID 1191 1191 Interchain (Probable).
FT DISULFID 1194 1194 Interchain (Probable).
FT DISULFID 1798 1798 Interchain (Probable).
FT CARBOHYD 251 251 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 371 371 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1086 1086 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1250 1250 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1309 1309 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1349 1349 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1500 1500 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 1799 AA, 196352 MW, 1728967A67AEDE33 CRC64;

Query Match 29.4%; Score 60; DB 1; Length 1799;
Best Local Similarity 29.8%; Pred. No. 1e+02;
Matches 14; Conservative 5; Mismatches 8; Indels 20; Gaps 3;

QY 5 YQGKCHCHM-----GTHCHSSD-GPRGVPEPRC 32
Db 1111 FTGQCHCHAGGGRTCEQELYWGDPLQCRACDCDPRG-IDKPOC 1156

RESULT 12
Q8ROYO PRELIMINARY; PRT; 1799 AA.
AC Q8ROYO
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Laminin, beta 2.
GN NamesLamb2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC STRAIN=Mix FVB/N;
RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marudina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Udell T.B., Toshitoki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RC SEQUENCE FROM N.A.
RC STRAIN=Mix FVB/N;
RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC026051; AAH26051.1; -.
DR HSSP; P02468; 1NPE.
DR MGD; MGI:99916; Lamb2.
DR GO; GO:0005578; C:extracellular matrix; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR005797; Cytb_b6_N.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR008979; Gal bind like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR008211; Laminin_N.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00053; Laminin_EGF; 13.
DR Pfam; PF00055; Laminin_N; 1.
DR PRINTS; PR00011; EGFLAMININ.
DR SMART; SM00180; EGF Lam; 13.
DR SMART; SM00136; LamNT; 1.
DR PROSITE; PS00192; CYTOCHROME_B_HEME; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; 10.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 12.
DR PROSITE; PS00119; PA2_ASP; UNKNOWN_1.
KW Laminin EGF-like domain.
SQ SEQUENCE 1799 AA, 196577 MW, 37CA24B9CDA0791F CRC64;

Query Match 29.4%; Score 60; DB 2; Length 1799;
Best Local Similarity 29.8%; Pred. No. 1e+02;
Matches 14; Conservative 5; Mismatches 8; Indels 20; Gaps 3;

QY 5 YQGKCHCHM-----GTHCHSSD-GPRGVPEPRC 32
Db 1111 FTGQCHCHAGGGRTCEQELYWGDPLQCRACDCDPRG-IDKPOC 1156

RESULT 13
LMB2_RAT
ID LMB2_RAT STANDARD; PRT; 1801 AA.
AC P15800;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Laminin beta-2 chain precursor (S-laminin) (Laminin chain B3).
GN Name=Lamb2;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RC SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=89159410; PubMed=2922051;
RA Hunter D.D., Shah V., Merlie J.P., Sanes J.R.;
RA "A laminin-like adhesive protein concentrated in the synaptic cleft of
RA the neuromuscular junction."
RL Nature 338:229-234(1989).
CC -!- FUNCTION: Binding to cells via a high affinity receptor, laminin
CC is thought to mediate the attachment, migration and organization
CC of cells into tissues during embryonic development by interacting
CC with other extracellular matrix components.
CC -!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
CC different polypeptide chains (alpha, beta, gamma), which are bound
CC to each other by disulfide bonds into a cross-shaped molecule

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; V01555; -; NOT_ANNOTATED_CDS.
DR PIR; A03742; Q0BEB3.
KW Early protein; Hypothetical protein; Repeat.
FT DOMAIN 149 648 4 X 125 AA TANDEM REPEATS.
FT REPEAT 149 273 1.
FT REPEAT 274 398 2.
FT REPEAT 399 523 3.
FT REPEAT 524 648 4.
FT REPEAT 660 AA; 66244 MW; 86DA1D67A37152A2 CRC64;
SQ SEQUENCE 660 AA; 29.2%; Score 59.5; DB 1; Length 660;
Query Match
Best Local Similarity 57.1%; Pred. No. 45;
Matches 12; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

Qy 13 MGHCHSSDQPRGVPEPRCP 33
Db 1 MGTPCQARGPR-TTLPHPCP 20

RESULT 15
Q777A3 PRELIMINARY; PRT; 660 AA.
AC Q777A3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE BHLF1 early reading frame.
OS Human herpesvirus 4 (Epstein-Barr virus).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Lymphocryptovirus.
OX NCBI_TaxID=10376;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B95-8;
RX MEDLINE=84270667; PubMed=6087149;
RA Baer R.J., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,
RA Gibson T.J., Hatfull G.F., Hudson G.S., Satchwell S.C., Seguin C.,
RA Tuffnell P.S., Barrell B.G.;
RT "DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";
RL Nature 310:207-211(1984).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=B95-8;
RX MEDLINE=84270667; PubMed=6087149;
RA Baer R.J., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,
RA Gibson T.J., Hatfull G.F., Hudson G.S., Satchwell S.C., Seguin C.,
RA Tuffnell P.S., Barrell B.G.;
RT "DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";
RL Nature 310:207-211(1984).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=B95-8;
RX MEDLINE=88283646; PubMed=2840285;
RA Laux G., Perricaudet M., Farrell P.J.;
RT "A spliced Epstein-Barr virus gene expressed in immortalized
RT lymphocytes is created by circularization of the linear viral
RT genome.";
RL EMBO J. 7:769-774(1988).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=B95-8;
RX MEDLINE=82014887; PubMed=6269066;
RA Arand J.R., Rymo L., Walsh J.E., Bjorck B., Lindahl T., Griffin B.E.;
RT "Molecular cloning of the complete Epstein-Barr virus genome as a set
RT of overlapping restriction endonuclease fragments.";
RL Nucleic Acids Res. 9:2999-3014(1981).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=B95-8;
RX MEDLINE=82059504; PubMed=7301588;
RA Kozak M.;
RT "Possible role of flanking nucleotides in recognition of the AUG
RT initiator codon by eukaryotic ribosomes.";

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RL Nucleic Acids Res. 9:5233-5252(1981).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=B95-8;
RX MEDLINE=83109311; PubMed=6296170;
RA Deininger P.L., Bankier A., Farrell P., Baer R., Barrell B.;
RT "Sequence analysis and in vitro transcription of portions of the
RT Epstein-Barr virus genome.";
RL J. Cell. Biochem. 19:267-274(1982).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=B95-8;
RX MEDLINE=83169725; PubMed=6300857;
RA Farrell P.J., Deininger P.L., Bankier A., Barrell B.;
RT "Homologous upstream sequences near Epstein-Barr virus promoters.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:1565-1569(1983).
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=B95-8;
RX MEDLINE=85035713; PubMed=6092825;
RA Bankier A.T., Deininger P.L., Farrell P.J., Barrell B.G.;
RT "Sequence analysis of the 17,166 base-pair EcoRI fragment C of B95-8
RT Epstein-Barr virus";
RL Mol. Biol. Med. 1:21-45(1983).
RN [8]
RP SEQUENCE FROM N.A.
RC STRAIN=B95-8;
RX MEDLINE=85060424;
RA Seguin C., Farrell P.J., Barrell B.G.;
RT "DNA sequence and transcription of the BamHI fragment B region of B95-
RT 8 Epstein-Barr virus.";
RL Mol. Biol. Med. 1:369-392(1983).
RN [9]
RP SEQUENCE FROM N.A.
RC STRAIN=B95-8;
RX MEDLINE=83294686; PubMed=6310141;
RA Jeang K.T., Hayward S.D.;
RT "Organization of the Epstein-Barr virus DNA molecule. III. Location of
RT the P3HR-1 deletion junction and characterization of the NotI repeat
RT units that form part of the template for an abundant 12-O-
RT tetradecanoylphorbol-13-acetate-induced mRNA transcript.";
RL J. Virol. 48:135-148(1983).
RN [10]
RP SEQUENCE FROM N.A.
RC STRAIN=B95-8;
RX MEDLINE=85060428; PubMed=6094955;
RA Bankier A.T., Deininger P.L., Satchwell S.C., Baer R., Farrell P.J.,
RA Barrell B.G.;
RT "DNA sequence analysis of the EcoRI Dhet fragment of B95-8 Epstein-
RT Barr virus containing the terminal repeat sequences.";
RL Mol. Biol. Med. 1:425-445(1983).
RN [11]
RP SEQUENCE FROM N.A.
RC STRAIN=B95-8;
RX MEDLINE=20331131; PubMed=10872327;
RA Farrell P.J., Bankier A., Seguin C., Deininger P., Barrell B.G.;
RT "Latent and lytic cycle promoters of Epstein-Barr virus.";
RL EMBO J. 2:1331-1338(1983).
RN [12]
RP SEQUENCE FROM N.A.
RC STRAIN=B95-8;
RX MEDLINE=84207939; PubMed=6327290;
RA Jones M.D., Foster L., Sheedy T., Griffin B.E.;
RT "The EB virus genome in Daudi Burkitt's lymphoma cells has a deletion
RT similar to that observed in a non-transforming strain (P3HR-1) of the
RT virus.";
RL EMBO J. 3:813-821(1984).
RN [13]
RP SEQUENCE FROM N.A.
RC STRAIN=B95-8;
RX MEDLINE=84236104; PubMed=6203743;
RA Biggin M., Farrell P.J., Barrell B.G.;
RT "Transcription and DNA sequence of the BamHI L fragment of B95-8

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RT Epstein-Barr virus.";
RL EMBL J. 3:1083-1090(1984).
RN [14]
RP SEQUENCE FROM N.A.
RC STRAIN=B95-8;
RX MEDLINE=84222045; PubMed=6328526;
RA Yates J., Warren N., Reisman D., Sugden B.;
RT "A cis-acting element from the Epstein-Barr viral genome that permits
RT stable replication of recombinant plasmids in latently infected
RT cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:3806-3810(1984).
RN [15]
RP SEQUENCE FROM N.A.
RC STRAIN=B95-8;
RX MEDLINE=84247360; PubMed=6330697;
RA Gibson T., Stockwell P., Ginsburg M., Barrell B.;
RT "Homology between two EBV early genes and HSV ribonucleotide reductase
RT and 38K genes.";
RL Nucleic Acids Res. 12:5087-5099(1984).
RN [16]
RP SEQUENCE FROM N.A.
RC STRAIN=B95-8;
RX MEDLINE=87289053; PubMed=3039467;
RA Bodescot M., Perricaudet M.;
RT "Clustered alternative splice sites in Epstein-Barr virus RNAs.";
RL Nucleic Acids Res. 15:5887-5887(1987).
RN [17]
RP SEQUENCE FROM N.A.
RC STRAIN=B95-8;
RX MEDLINE=91021036; PubMed=2171209;
RA Parker B.D., Bankier A., Satchwell S., Barrell B., Farrell P.J.;
RT "Sequence and transcription of Raji Epstein-Barr virus DNA spanning
RT the B95-8 deletion region.";
RL Virology 179:339-346(1990).
RN [18]
RP SEQUENCE FROM N.A.
RC STRAIN=B95-8;
RX Hatfull G.F., Barrell B.G., Quinn J., McGeoch D.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
RN [19]
RP SEQUENCE FROM N.A.
RC STRAIN=B95-8;
RA Binne U.K., Amon W., Farrell P.J.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ507799; CAD53473.1; -.
SQ SEQUENCE 660 AA; 66244 MW; 86DA1D67A37152A2 CRC64;

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Query Match      29.2%; Score 59.5; DB 2; Length 660;
Best Local Similarity 57.1%; Pred. No. 45;
Matches 12; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

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QY      13 MGHCHSSDGRGVIPRCP 33
Db      1 MGTFCQARGPR-TTPLPHCP 20

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Search completed: November 16, 2004, 19:14:36  
Job time : 40.0515 secs

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OM protein - protein search, using sw model

Run on: November 16, 2004, 17:12:10 ; Search time 35.1008 Seconds  
(without alignments)  
337.259 Million cell updates/sec

Title: US-10-036-444-6

Perfect score: 204

Sequence: 1 STVYVQKCHCHGTHCHSSDGRGVIPFRCP 33

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 200273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_23Sep04:\*  
1: Geneseq1980s:\*  
2: Geneseq1990s:\*  
3: Geneseq2000s:\*  
4: Geneseq2001s:\*  
5: Geneseq2002s:\*  
6: Geneseq2003as:\*  
7: Geneseq2003bs:\*  
8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	204	100.0	33	4 AAE02773	Aae02773 Human Nkp
2	204	100.0	33	8 ADQ30926	Adq30926 Human Nkp
3	204	100.0	190	2 AAY06401	Aay06401 Human B-C
4	204	100.0	190	4 AAE02769	Aae02769 Human Nkp
5	204	100.0	190	8 ADO19810	Ado19810 Human PRO
6	204	100.0	190	8 ADQ30923	Adq30923 Human Nkp
7	61.5	30.1	82	3 AAG35071	Aag35071 Arabidops
8	61.5	30.1	82	3 AAG11882	Aag11882 Arabidops
9	61.5	30.1	636	4 AAB66269	Aab66269 Rat TANGO
10	60	29.4	66	4 AAO10665	Aao10665 Human pol
11	60	29.4	201	2 AAY06403	Aay06403 Human B-C
12	60	29.4	1799	5 AAM50359	Aam50359 Mouse lam
13	60	29.4	1801	2 AAW50895	Aaw50895 Rat lamin
14	60	29.4	1801	7 ADE60383	Ade60383 Rat Prote
15	59	28.9	57	4 AAU43863	Aau43863 Propionib
16	59	28.9	57	6 ABM40382	Abm40382 Propionib
17	59	28.9	2813	2 AAW54347	Aaw54347 Canine vo
18	59	28.9	2813	3 AAY70557	Aay70557 Canine vo
19	58.5	28.7	77	5 ABB97268	Abb97268 Novel hum
20	58.5	28.7	148	2 AAY74028	Aay74028 Human pro
21	58.5	28.7	148	4 AAG74543	Aag74543 Human col
22	58.5	28.7	302	4 AEG03692	Aeg03692 Novel hum
23	58.5	28.7	2469	5 AAE18207	Aae18207 Human MOL
24	58.5	28.7	2469	7 ADD18192	Add18192 Human mol
25	58.5	28.7	2471	2 AAO27065	Aao27065 Human Not

#### ALIGNMENTS

RESULT 1

AAE02773

ID AAE02773 standard; peptide; 33 AA.

XX

AC AAE02773;

XX

DT 06-AUG-2001 (first entry)

XX

DE Human Nkp30 receptor intracellular region sequence.

XX

XX Human; Nkp30 receptor; natural killer cell; cytostatic; antimicrobial;  
KW melanoma; hepatocarcinoma; lung adenocarcinoma; viral infection; tumour;  
KW immunosuppressant; antiviral; drug; grafting enhancement; leukaemia;  
KW therapy; intracellular region.

XX

OS Homo sapiens.

XX

PN WO200136630-A2.

XX

PD 25-MAY-2001.

XX

PF 15-NOV-2000; 2000WO-EP011697.

XX

PR 15-NOV-1999; 95CA-02288307.

XX

PR 15-NOV-1999; 99US-00440514.

XX

PA (INNA-) INNATE PHARMA SAS.

XX

PA (UYGE-) UNIV GENOVA.

XX

PI Moretta A, Bottino C, Biassoni R;

XX

PI WPI; 2001-329221/34.

XX

XX NK cells, comprises the amino acid sequences of the Nkp30 molecule.

XX

PS Claim 1; Fig 7B; 83pp; English.

XX

XX The invention relates to human Nkp30 receptor and its corresponding cDNA  
molecule which is involved in natural cytotoxicity mediated by natural  
killer (NK) cells and antibodies that identify the same. Nkp30 receptor  
is a member of immunoglobulin super family (Ig-SF). Nkp30 is selectively  
expressed on the surface of human mature NK cells. Nkp30 and its cDNA are  
useful for detecting and/or quantifying the presence of NK cells in a  
biological sample. The invention also provide kits for detecting and/or  
quantifying the presence of NK cells, for the selective removal of NK  
cells from a biological sample, for the positive and selective  
purification of NK cells from a biological sample and for the in vitro

Aay06816 Human Not  
Aag79774 Human Not  
Abp72572 Human Not  
Abr61831 Human Not  
Abr61760 Human Not  
Ade58245 Human Pro  
Ade63707 Human Pro  
Ade63703 Human Pro  
Ade63715 Human Pro  
Ade63711 Human Pro  
Adl26913 Human Not  
Adm41517 Human Not  
Adn30468 Human Not  
Adp67249 Human Not  
Ade62175 Transcript  
Aaw25717 Mouse gam  
Abb57371 Mouse lsc  
Adf42806 Mouse MDC  
Abb66756 Drosophil  
Adk34463 Novel hum

26 58.5 28.7 2471 2' AAY06816  
27 58.5 28.7 2471 6 AAG79774  
28 58.5 28.7 2471 6 ABP72572  
29 58.5 28.7 2471 6 ABR61831  
30 58.5 28.7 2471 7 ABR61760  
31 58.5 28.7 2471 7 ADE58245  
32 58.5 28.7 2471 7 ADE63707  
33 58.5 28.7 2471 7 ADE63703  
34 58.5 28.7 2471 7 ADE63715  
35 58.5 28.7 2471 7 ADE63711  
36 58.5 28.7 2471 8 ADL26913  
37 58.5 28.7 2471 8 ADM41517  
38 58.5 28.7 2471 8 ADN30468  
39 58.5 28.7 2471 8 ADP67249  
40 58 28.4 180 8 ADE62175  
41 58 28.4 845 2 AAW25717  
42 58 28.4 845 5 ABB57371  
43 58 28.4 845 8 ADF42806  
44 57.5 28.2 434 4 ABB66756  
45 56.5 27.7 292 5 ADK34463

CC stimulation of NK cell cytotoxicity. The invention further provides a  
 CC pharmaceutical composition which is used as a drug for grafting  
 CC enhancement, graft versus host (GVH) inhibition, stimulation of graft  
 CC versus tumour (GVT) and especially graft versus leukaemia (GvL), and for  
 CC the prevention, palliation and/or therapy of solid or liquid tumours,  
 CC such as melanoma, hepatocarcinoma and lung adenocarcinoma, and/or  
 CC microorganism, notably viral infection. Nkp30 antibodies are useful for  
 CC identifying Nkp30 natural ligands and allow assessment of the level of  
 CC surface Nkp30 ligand expressed on an NK-susceptible target cell and the  
 CC comparison of this level to the standard physiological one. Hence Nkp30  
 CC antibodies are useful in the diagnosis of tumours or of infection. The  
 CC present sequence is the intracellular region of human Nkp30 receptor  
 XX  
 SQ Sequence 33 AA;

Query Match 100.0%; Score 204; DB 4; Length 33;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-17; Indels 0; Gaps 0;  
 Matches 33; Conservative 0; Mismatches 0;

Oy 1 STVYQKCHCHMGTHCHSSDGRGVIPERCP 33  
 |||||  
 Db 1 STVYQKCHCHMGTHCHSSDGRGVIPERCP 33

## RESULT 2

ADQ30926  
 ID ADQ30926 standard; protein; 33 AA.

XX  
 AC ADQ30926;

DT 23-SEP-2004 (first entry)

XX  
 DE Human Nkp30 cytoplasmic tail.

XX Natural killer cell; NK cell; Nkp30; cytostatic; antimicrobial.

OS Homo sapiens.

XX W02004056392-A1.

PN 08-JUL-2004.

XX 22-DEC-2003; 2003WO-EP014716.

XX 23-DEC-2002; 2002US-0435344P.

XX (INNA-) INNATE PHARMA.

XX Romagne F, Andre P;

XX WPI; 2004-507595/48.

XX Pharmaceutical compositions that stimulate proliferation of natural  
 PT killer cells useful for therapy of melanoma, chronic myeloid, and  
 PT leukemia, comprise an anti-natural killer cell receptor antibody and  
 PT interleukins.

PS Claim 3; SEQ ID NO 4; 35pp; English.

XX The present sequence is that of the cytoplasmic tail of human Nkp30  
 CC ADQ30923, a 190 amino acid polypeptide that is selectively expressed by  
 CC natural killer (NK) cells, and particularly by mature NK cells. Claimed  
 CC pharmaceutical compositions that have a stimulating effect on the  
 CC proliferation of NK cells comprise an antibody such as an anti-Nkp30  
 CC antibody or anti-Nkp46 antibody or its immuno-reactive fragment and a  
 CC cytokine selected from interleukin-2 (IL2), IL12, IL15 and IL21, the  
 CC antibody(ies) and cytokine(s) being administered together or separately  
 CC to a subject. The anti-Nkp30 antibody is an isolated antibody or its  
 CC antigen-binding fragment which specifically binds to Nkp30 or to a  
 CC fragment, including the cytoplasmic tail, of Nkp30. The pharmaceutical  
 CC compositions, when used for daily subcutaneous injection, comprising from  
 CC 1 ng to 100 mg/kg (body weight) of antibody(ies), and lower than 1  
 CC million units/square meters/day of cytokine(s), are useful for the

CC prevention, palliation and therapy of e.g. melanoma, chronic myeloid  
 CC leukaemia, acute myeloid leukaemia, lymphoma, multiple myeloma,  
 CC hepatocarcinoma, lung adenocarcinoma, neuroblastoma and for antimicrobial  
 CC prevention, palliation and therapy (claimed).

XX Sequence 33 AA;

Query Match 100.0%; Score 204; DB 8; Length 33;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-17;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 STVYQKCHCHMGTHCHSSDGRGVIPERCP 33  
 |||||  
 Db 1 STVYQKCHCHMGTHCHSSDGRGVIPERCP 33

## RESULT 3

AY06401  
 ID AY06401 standard; protein; 190 AA.

XX  
 AC AY06401;

XX 20-SEP-1999 (first entry)

XX Human B-cell myelin oligodendrocyte glycoprotein BMOG.

XX MBOG; B-cell myelin oligodendrocyte glycoprotein; human;  
 KW signal transduction; immunomodulator; antiinflammatory;  
 KW autoimmune disease; inflammation; gene therapy; diagnosis.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..12

FT Protein /note= "leader peptide"

FT Modified-site 13..190

FT Modified-site /note= "mature protein"

FT Modified-site 42

FT Modified-site /note= "N-glycosylated"

FT Modified-site 68

FT Modified-site /note= "N-glycosylated"

FT Domain 121

FT Domain 139..162

FT Peptide /note= "transmembrane domain"

FT Peptide 166..190

XX /note= "alternatively spliced C-terminal end"

XX W09923867-A2.

XX 20-MAY-1999.

XX 05-NOV-1998; 98WO-US023826.

XX 07-NOV-1997; 97US-0064761P.

XX (BIOJ) BIOGEN INC.

XX Browning J;

XX WPI; 1999-418423/35.

XX N-PSDB; AAX59347.

XX Novel B-cell myelin oligodendrocyte glycoproteins.

PS Claim 2; Page 42; 43pp; English.

XX This sequence represents human BMOG, a novel member of the B cell myelin  
 CC oligodendrocyte glycoprotein family that is expressed by germinal centre  
 CC B cells. 3 C-terminal splice variants (see AY06401-03) of BMOG were  
 CC identified. The protein is present primarily in the spleen, in lymph  
 CC nodes and in germinal centre B cells. It may have immunoregulatory  
 CC functions, and soluble or chimeric fusion proteins of BMOG may be used to

CC regulate the immune system in autoimmune or inflammatory disease. Vectors  
CC comprising BMOG, prokaryotic and eukaryotic host cells, and a method of  
CC producing BMOG using these transformed host cells are also provided. BMOG  
CC polypeptides can be used for modulating the immune system of a subject or  
CC to inhibit signal transduction in a cell expressing BMOG by contacting it  
CC with a soluble BMOG protein. The nucleic acid can be used for gene  
CC therapy. The protein can also be used to target a toxin, imaging agent or  
CC radionuclide to a cell expressing BMOG. (All claimed)  
XX  
SQ Sequence 190 AA;

Query Match 100.0%; Score 204; DB 2; Length 190;  
Best Local Similarity 100.0%; Pred. No. 6.9e-17;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 STVYQKCHCHMGTHCHSSDGRGVIPEPRCP 33  
DB 158 STVYQKCHCHMGTHCHSSDGRGVIPEPRCP 190

RESULT 4  
AAE02769  
ID AAE02769 standard; protein; 190 AA.  
XX  
AC AAE02769;  
XX  
DT 06-AUG-2001 (first entry)  
XX  
DE Human NKp30 receptor.  
XX  
KW Human; NKp30 receptor; natural killer cell; cytostatic; antimicrobial;  
KW melanoma; hepatocarcinoma; lung adenocarcinoma; viral infection; tumour;  
KW immunosuppressant; antiviral; drug; grafting enhancement; leukaemia;  
KW therapy.  
XX  
OS Homo sapiens.

Key Location/Qualifiers  
FT Peptide 1..118  
FT /label= Signal\_peptide  
FT Protein 19..190  
FT /label= Mature\_NKp30\_receptor\_protein  
FT Region 19..138  
FT /label= Extracellular\_region  
FT /note= "Forms an immunoglobulin (Ig) V-like domain"  
FT Modified-site 42  
FT /note= "N-glycosylation site"  
FT Modified-site 121  
FT /note= "N-glycosylation site"  
FT Region 139..157  
FT /label= Transmembrane\_region  
FT Region 158..190  
FT /label= Intracellular\_region

XX WO200136630-A2.  
XX  
XX 25-MAY-2001.  
XX  
XX 15-NOV-2000; 2000WO-EP011597.  
XX  
XX 15-NOV-1999; 99CA-02288307.  
XX 15-NOV-1999; 99US-00440514.  
XX  
XX (INNA-) INNATE PHARMA SAS.  
XX (UYGE-) UNIV GENOVA.  
XX  
XX Moretta A, Bottino C, Biassoni R;  
XX  
XX WPI; 2001-329221/34.  
XX N-PSDB; AAD06564.  
XX

PT Novel compound, useful for detection and/or quantifying the presence of  
PT NK cells, comprises the amino acid sequences of the NKp30 molecule.

XX  
PS  
XX Claim 1; Fig 7B; 83pp; English.  
CC The invention relates to human NKp30 receptor and its corresponding cDNA  
CC molecule which is involved in natural cytotoxicity mediated by natural  
CC killer (NK) cells and antibodies that identify the same. NKp30 receptor  
CC is a member of immunoglobulin super family (Ig-SF). NKp30 is selectively  
CC expressed on the surface of human mature NK cells. NKp30 and its cDNA are  
CC useful for detecting and/or quantifying the presence of NK cells in a  
CC biological sample. The invention also provide kits for detecting and/or  
CC quantifying the presence of NK cells, for the selective removal of NK  
CC cells from a biological sample, for the positive and selective  
CC purification of NK cells from a biological sample and for the in vitro  
CC stimulation of NK cell cytotoxicity. The invention further provides a  
CC pharmaceutical composition which is used as a drug for grafting  
CC enhancement, graft versus host (GvH) inhibition, stimulation of graft  
CC versus tumour (GvT) and especially graft versus leukaemia (GvL), and for  
CC the prevention, palliation and/or therapy of solid or liquid tumours,  
CC such as melanoma, hepatocarcinoma and lung adenocarcinoma, and/or  
CC microorganism, notably viral infection. NKp30 antibodies are useful for  
CC identifying NKp30 natural ligands and allow assessment of the level of  
CC surface NKp30 ligand expressed on an NK-susceptible target cell and the  
CC comparison of this level to the standard physiological one. Hence NKp30  
CC antibodies are useful in the diagnosis of tumours or of infection. The  
CC present sequence is human NKp30 receptor  
XX

SQ Sequence 190 AA;  
Query Match 100.0%; Score 204; DB 4; Length 190;  
Best Local Similarity 100.0%; Pred. No. 6.9e-17;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 STVYQKCHCHMGTHCHSSDGRGVIPEPRCP 33  
DB 158 STVYQKCHCHMGTHCHSSDGRGVIPEPRCP 190

RESULT 5  
AD019810  
ID AD019810 standard; protein; 190 AA.  
XX  
AC AD019810;  
XX  
DT 12-AUG-2004 (first entry)  
XX  
DE Human PRO polypeptide #367.  
XX  
KW Human; PRO; immune related disorder; systemic lupus erythematosus;  
KW rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;  
KW systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;  
KW autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;  
KW diabetes mellitus; renal disease; demyelinating disease;  
KW central nervous system; peripheral nervous system;  
KW demyelinating polyneuropathy; Guillain-Barre syndrome;  
KW chronic inflammatory demyelinating polyneuropathy.

XX Homo sapiens.  
XX  
XX WO2004043361-A2.  
XX  
XX 27-MAY-2004.  
XX  
XX 06-NOV-2003; 2003WO-US035268.  
XX  
XX 08-NOV-2002; 2002US-0425235P.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;  
XX Wood WI, Wu TD;  
XX  
XX WPI; 2004-420067/39.  
XX N-PSDB; AD019809.

XX Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for  
 PT treating an immune related disorder such as systemic lupus erythematosus,  
 PT rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or  
 PT spondyloarthritis.  
 XX Claim 7; SEQ ID NO 734; 1731pp; English.

XX The invention relates to human PRO polypeptides and the polynucleotides  
 CC encoding them. The polypeptides and polynucleotides are useful for  
 CC treating and diagnosing immune related disorders in mammals. The immune  
 CC related disorders include systemic lupus erythematosus, rheumatoid  
 CC arthritis, osteoarthritis, juvenile chronic arthritis, systemic  
 CC sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune  
 CC haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes  
 CC mellitus, immune-mediated renal disease, demyelinating diseases of the  
 CC central or peripheral nervous system, demyelinating polyneuropathy,  
 CC Guillain-Barre syndrome and chronic inflammatory demyelinating  
 CC polyneuropathy. This sequence represents a human PRO polypeptide of the  
 CC invention.

XX SQ Sequence 190 AA;  
 Query Match 100.0%; Score 204; DB 8; Length 190;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-17;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STVYQKCHCHMGTHCHSSDGRGVIPERCP 33  
 Db 158 STVYQKCHCHMGTHCHSSDGRGVIPERCP 190

RESULT 6  
 ADQ30923  
 ID ADQ30923 standard; protein; 190 AA.  
 XX AC ADQ30923;  
 XX DT 23-SEP-2004 (first entry)  
 XX DE Human NKp30 polypeptide.  
 XX KW Natural killer cell; NK cell; NKp30; cytostatic; antimicrobial.  
 XX OS Homo sapiens.  
 XX PH Location/Qualifiers  
 FT Region 19..138  
 FT /label= Extracellular region  
 FT /note= "Region specifically described in Claim 3"  
 FT Region 20..133  
 FT /label  
 FT /note= "Immunogenic peptide specifically described in  
 FT Claim 3"  
 FT Region 139..157  
 FT /label= Transmembrane region  
 FT /note= "Region specifically described in Claim 3"  
 FT Region 158..190  
 FT /label= Cytoplasmic tail  
 FT /note= "Region specifically described in Claim 3"  
 XX WO2004056392-A1.  
 XX 08-JUL-2004.  
 XX 22-DEC-2003; 2003WO-EP014716.  
 XX 23-DEC-2002; 2002US-0435344P.  
 XX (INNA-) INNATE PHARMA.  
 XX Romagne F, Andre P;

DR WPI; 2004-507595/48.  
 XX Pharmaceutical compositions that stimulate proliferation of natural  
 PT killer cells useful for therapy of melanoma, chronic myeloid, and  
 PT leukemia, comprise an anti-natural killer cell receptor antibody and  
 PT interleukins.  
 XX Claim 3; SEQ ID NO 1; 35pp; English.

XX The present sequence is that of human NKp30, a 190 amino acid polypeptide  
 CC (about 30 kDa on SDS-PAGE) that is selectively expressed by natural  
 CC killer (NK) cells, and particularly by mature NK cells. Claimed  
 CC pharmaceutical compositions that have a stimulating effect on the  
 CC proliferation of NK cells comprise an antibody such as an anti-NKp30  
 CC antibody or anti-NKp46 antibody or its immuno-reactive fragment and a  
 CC cytokine selected from interleukin-2 (IL2), IL12, IL15 and IL21, the  
 CC antibody(ies) and cytokine(s) being administered together or separately  
 CC to a subject. The anti-NKp30 antibody is an isolated antibody or its  
 CC antigen-binding fragment which specifically binds to NKp30 or to a  
 CC fragment ADQ30924-ADQ30927 of NKp30. The pharmaceutical compositions,  
 CC when used for daily subcutaneous injection, comprising from 1 ng to 100  
 CC mg/kg (body weight) of antibody(ies), and lower than 1 million  
 CC units/square meters/day of cytokine(s), are useful for the prevention,  
 CC palliation and therapy of e.g. melanoma, chronic myeloid leukaemia, acute  
 CC myeloid leukaemia, lymphoma, multiple myeloma, hepatocarcinoma, lung  
 CC adenocarcinoma, neuroblastoma and for antimicrobial prevention,  
 CC palliation and therapy (claimed).

XX SQ Sequence 190 AA;  
 Query Match 100.0%; Score 204; DB 8; Length 190;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-17;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STVYQKCHCHMGTHCHSSDGRGVIPERCP 33  
 Db 158 STVYQKCHCHMGTHCHSSDGRGVIPERCP 190

RESULT 7  
 AG35071  
 ID AG35071 standard; protein; 82 AA.  
 XX AC AG35071;  
 XX DT 18-OCT-2000 (first entry)  
 XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 42786.  
 XX KW Protein identification; signal transduction pathway; metabolic pathway;  
 KW hybridisation assay; genetic mapping; gene expression control; promoter;  
 KW termination sequence.  
 XX OS Arabidopsis thaliana.  
 XX EP1033405-A2.  
 XX 06-SEP-2000.  
 XX 25-FEB-2000; 2000EP-00301439.  
 XX 25-FEB-1999; 99US-0121825P.  
 XX 05-MAR-1999; 99US-0123180P.  
 XX 09-MAR-1999; 99US-0123548P.  
 XX 23-MAR-1999; 99US-0125788P.  
 XX 25-MAR-1999; 99US-0126264P.  
 XX 29-MAR-1999; 99US-0126785P.  
 XX 01-APR-1999; 99US-0127462P.  
 XX 06-APR-1999; 99US-0128234P.  
 XX 08-APR-1999; 99US-0128714P.  
 XX 16-APR-1999; 99US-0129845P.  
 XX 19-APR-1999; 99US-0130077P.  
 XX 21-APR-1999; 99US-0130449P.





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PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159564P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161931P.
PR 28-OCT-1999; 99US-0162142P.

Query Match 30.1%; Score 61.5; DB 3; Length 82;
Best Local Similarity 52.4%; Pred. No. 6.5;
Matches 11; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

QY 3 VYQKCHCHMGTHCHSSDCP 23
Db 48 LFSDGKCH-HLKLHCGSSHP 67

RESULT 8
AAG11882
ID AAG11882 standard; protein; 82 AA.
XX AC AAG11882;
XX DT 17-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 10773.
XX KW Protein identification; signal transduction pathway; metabolic pathway;
XX KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX KW termination sequence.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-00301439.
XX PR 25-FEB-1999; 99US-0121825P.
XX PR 05-MAR-1999; 99US-0123180P.
XX PR 09-MAR-1999; 99US-0123548P.
XX PR 23-MAR-1999; 99US-0125788P.
XX PR 25-MAR-1999; 99US-0126264P.
XX PR 29-MAR-1999; 99US-0126785P.
XX PR 01-APR-1999; 99US-0127462P.
XX PR 06-APR-1999; 99US-0128234P.
XX PR 08-APR-1999; 99US-0128714P.
XX PR 16-APR-1999; 99US-0129845P.
XX PR 19-APR-1999; 99US-0130077P.
XX PR 21-APR-1999; 99US-0130449P.
XX PR 23-APR-1999; 99US-0130510P.
XX PR 28-APR-1999; 99US-0130891P.
XX PR 30-APR-1999; 99US-0131449P.
XX PR 30-APR-1999; 99US-0132048P.
XX PR 04-MAY-1999; 99US-0132407P.
XX PR 04-MAY-1999; 99US-0132484P.
XX PR 05-MAY-1999; 99US-0132485P.
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PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144086P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144332P.
PR 20-JUL-1999; 99US-0144632P.
PR 21-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145087P.
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PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145132P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148117P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148585P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149733P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151085P.
PR 27-AUG-1999; 99US-0151086P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159223P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 18-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.

PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 30.1%; Score 61.5; DB 3; Length 82;
Best Local Similarity 52.4%; Pred. No. 6.5;
Matches 11; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

QY 3 VYVQKCHCHMGTHCHSSDGP 23
   : : : : : : : : : : : : : :
Db 48 LPSDGKCH-HLKLHCGSSHGP 67

RESULT 9
AAB66269
ID AAB66269 standard; protein; 636 AA.
XX
AC AAB66269;
XX
DT 05-APR-2001 (first entry)
XX
DE Rat TANGO 272 SEQ ID NO: 20.
XX
KW Membrane associated protein; secreted protein; human; mouse; rat;
KW INTERCEPT 340; MANGO 003; MANGO 347; TANGO 272; TANGO 295; TANGO 354;
KW TANGO 378; skeletal disorder; cardiovascular disorder; renal disorder;
KW haematopoietic disorder; neural disorder; hepatic disorder;
KW neoplastic disease.
XX
OS Rattus sp.
XX
PN WO200100673-A1.
XX
PD 04-JAN-2001.
XX
PF 29-JUN-2000; 2000WO-US018198.
XX
PR 30-JUN-1999; 99US-00345464.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Barnes TM, Fraser CC, Wrighton N, Myers P, Busfield SJ, Sharp JD;
XX WPI; 2001-050128/06.
XX N-PSDB; AAP27791.
XX
PT Isolated secreted or transmembrane proteins are used for diagnosis and
PT treatment of neoplastic and hematopoietic disorders e.g. T cell
XX disorders, cancer and tumors.
XX
PS Claim 9; Page 238-240; 294pp; English.
XX
CC The present invention provides the protein and coding sequences for a
CC number of membrane associated and secreted proteins from human, mouse and
CC rat. The proteins are designated INTERCEPT 340, MANGO 003, MANGO 347,
CC TANGO 272, TANGO 295, TANGO 254 and TANGO 378. The proteins are all
CC involved in signal transduction and the sequences can be used in the
CC treatment of cardiovascular, renal, hepatic, neural, neoplastic, skeletal
CC and haematopoietic disorders
XX
SQ Sequence 636 AA;
```

Query Match 30.1%; Score 61.5; DB 4; Length 636;  
Best Local Similarity 44.4%; Pred. No. 49;  
Matches 12; Conservative 0; Mismatches 12; Indels 3; Gaps 1;  
Qy 9 CHCHGTHCHSSDGRGVIP---EPRC 32  
Db 411 CQCHGATCPDQSGVCVCPGWTGPNC 437

RESULT 10  
AAO10665  
ID AAO10665 standard; protein; 66 AA.  
XX AAO10665;  
AC AAO10665;  
XX 06-NOV-2001 (first entry)  
XX Human polypeptide SEQ ID NO 24557.  
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
XX vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
XX tissue growth factor; immunomodulatory; cancer; leukaemia;  
XX nervous system disorders; arthritis; inflammation.  
XX Homo sapiens.  
XX WO200164835-A2.  
XX 07-SEP-2001.  
XX 26-FEB-2001; 2001WO-US004927.  
XX 28-FEB-2000; 2000US-00515126.  
XX 18-MAY-2000; 2000US-00577409.  
XX (HYSE-) HYSEQ INC.  
XX Tang YT, Liu C, Drmanac RT;  
XX WPI; 2001-514838/56.  
XX N-PSDB; AA190596.

Isolated nucleic acids and polypeptides, useful for preventing diagnosing  
and treating e.g. leukemia, inflammation and immune disorders.  
Claim 20; SEQ ID NO 24557; 1399pp + Sequence Listing, English.  
The invention relates to human polynucleotides (AA179941-AA193841) and  
the encoded proteins (AAO00010-AAO1910) that exhibit activity relating to  
cytokine, cell proliferation or cell differentiation or which may induce  
production of other cytokines in other cell populations. The  
polynucleotides and polypeptides are useful in gene therapy, vaccines or  
peptide therapy. The polypeptides have various cytokine-like activities,  
e.g. stem cell growth factor activity, haematopoiesis regulating  
activity, tissue growth factor activity, immunomodulatory activity and  
activin/inhibin activity, and may be useful in the diagnosis and/or  
treatment of cancer, leukaemia, nervous system disorders, arthritis and  
inflammation. Note: The sequence data for this patent did not form part  
of the printed specification, but was obtained in electronic format  
directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

Sequence 66 AA;  
Query Match 29.4%; Score 60; DB 4; Length 66;  
Best Local Similarity 37.0%; Pred. No. 7.9;  
Matches 10; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

Qy 4 YYQKCHCHGTHCHSSDGRGVIP 30  
Db 27 HHHHCHCHVSHHHNSQHPPPPPP 53

RESULT 11  
AAO06403  
ID AAY06403 standard; protein; 201 AA.  
XX AAY06403;  
AC AAY06403;  
XX 20-SEP-1999 (first entry)  
XX Human B-cell myelin oligodendrocyte glycoprotein BMOG.  
XX BMOG; B-cell myelin oligodendrocyte glycoprotein; human;  
XX signal transduction; immunomodulator; antiinflammatory;  
XX autoimmune disease; inflammation; gene therapy; diagnosis.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
FH Peptide 1..12  
FT /note= "leader peptide"  
FT Protein 13..201  
FT /note= "mature protein"  
FT Modified-site 42  
FT /note= "N-glycosylated"  
FT Modified-site 68  
FT /note= "N-glycosylated"  
FT Modified-site 121  
FT /note= "N-glycosylated"  
FT Domain 139..162  
FT /note= "transmembrane domain"  
FT Peptide 166..201  
FT /note= "alternatively spliced C-terminal end"  
XX WO9923867-A2.  
XX 20-MAY-1999.  
XX 05-NOV-1998; 98WO-US023826.  
XX 07-NOV-1997; 97US-0064761P.  
XX (BIOJ ) BIOGEN INC.  
XX Browning J;  
XX WPI; 1999-418423/35.  
XX N-PSDB; AAX59349.  
XX Novel B-cell myelin oligodendrocyte glycoproteins.  
XX Claim 2; Page 43; 43pp; English.  
This sequence represents human BMOG, a novel member of the B cell myelin  
oligodendrocyte glycoprotein family that is expressed by germinal centre  
B cells. 3 C-terminal splice variants (see AAY06401-03) of BMOG were  
identified. The protein is present primarily in the spleen, in lymph  
nodes and in germinal centre B cells. It may have immunoregulatory  
functions, and soluble or chimeric fusion proteins of BMOG may be used to  
regulate the immune system in autoimmune or inflammatory disease. Vectors  
comprising BMOG, prokaryotic and eukaryotic host cells, and a method of  
producing BMOG using these transformed host cells are also provided. BMOG  
polypeptides can be used for modulating the immune system of a subject or  
to inhibit signal transduction in a cell expressing BMOG by contacting it  
with a soluble BMOG protein. The nucleic acid can be used for gene  
therapy. The protein can also be used to target a toxin, imaging agent or  
radioconclide to a cell expressing BMOG. (All claimed)

Sequence 201 AA;  
Query Match 29.4%; Score 60; DB 2; Length 201;  
Best Local Similarity 43.2%; Pred. No. 24;  
Matches 16; Conservative 2; Mismatches 7; Indels 12; Gaps 2;

Qy 1 STVYQKCHCHGTHCHSSDGRP----GVIPRCP 33

Db 158 STVYQK-----CLTWGRRQLPAVVPAPLP 186

RESULT 12  
AAW50359  
ID AAW50359 standard; protein; 1799 AA.  
XX AC AAW50359;  
XX DT 18-FEB-2002 (first entry)  
XX DE Mouse laminin-15 beta 2 chain.  
XX KW Laminin-15; mouse; retina; eye; therapy; ophthalmological;  
XX KW antinflammatory; rod dystrophy; rod-cone dystrophy;  
XX KW retinitis pigmentosa; macular degeneration; retinal detachment.  
XX OS Mus musculus.  
XX PN WO2C0183516-A1.  
XX PD 08-NOV-2001.  
XX PF 01-MAY-2001; 2001WO-US013943.  
XX PR 01-MAY-2000; 2000US-0200863P.  
XX PA (MASS-) MASSACHUSETTS GEN HOSPITAL.  
XX PI Burgeson RE, Brunken W, Champlaud M, Hunter D;  
XX DR WPI; 2002-041478/05.  
XX PT Novel substantially pure preparation comprising laminin having laminin  
PT chain alpha 5, beta 2, and gamma 3, useful for treating retinal disorders  
PT such as retinitis pigmentosa, macular degeneration, retinal detachment.  
XX PS Disclosure; Fig 3A; 58pp; English.

The present sequence is that of the beta 2 chain of mouse laminin-15, a novel member of the laminin family that is produced in the retina. The retina produces 2 novel laminin trimers: laminin-14 (alpha 4, beta 2, gamma 3) and laminin-15 (alpha 5, beta 2, gamma 3). These are expressed within the inter-photoreceptor matrix and in the outer plexiform layer, and may serve to stabilise retinal synapses. The invention provides laminin-15 preparations and cells comprising a nucleic acid encoding the laminin alpha 5, beta 2 and gamma 3 chains, and which are capable of producing laminin-15. The laminin-15 preparation is used in claimed methods of: increasing retina immunophotoreceptor matrix stability; increasing the stability of retina photoreceptor compounds, especially an outer segment, inner segment or synapse; increasing retina adhesion; treating a disorder associated with retina degeneration, especially rod dystrophy, rod-cone dystrophy, retinitis pigmentosa, macular degeneration and retinal detachment; increasing the stability of synapses of the central nervous system or peripheral nervous system; stimulating neuroregeneration, axon outgrowth or synapse formation; preparing an implant, e.g. a catheter, artificial joint, retinal implant, timed releasing device, neural cell growth guide or artificial tissue, by coating with the laminin-15 preparation; and increasing photosensitivity by implanting a tip coated with the laminin-15 preparation into an eye. The laminin may be recombinant, and the 3 chains co-expressed in the same cell or expressed in different cells

SQ Sequence 1799 AA;  
Query Match 29.4%; Score 60; DB 5; Length 1799;  
Best Local Similarity 29.8%; Pred. No. 2.1e+02;  
Matches 14; Conservative 5; Mismatches 8; Indels 20; Gaps 3;  
QY 5 YQKCHCHM-----GTHCHSSD-GPRGVIEPRC 32  
DB 1111 FTGQCHCHAGRGRCBCELYWGDPELQCRACDCDPRG-IDKPOC 1156

RESULT 13  
AAW50895  
ID AAW50895 standard; protein; 1801 AA.  
XX AC AAW50895;  
XX DT 07-DEC-1998 (first entry)  
XX DE Rat laminin B2 chain.  
XX KW Laminin; rat; beta-amyloid; amyloidosis; Alzheimer's disease;  
KW Down's syndrome; hereditary cerebral haemorrhage; inflammation;  
KW malignancy; Familial Mediterranean Fever; multiple myeloma;  
KW type II diabetes; prion disease; Creutzfeldt-Jacob disease; CJD;  
KW Gerstmann-Strausler syndrome; kuru; scrapie; haemodialysis;  
KW carpal tunnel syndrome; senile cardiac amyloid polynuropathy;  
KW Familial Amyloidotic Polynuropathy; thyroid carcinoma; diagnosis;  
KW therapy.  
XX OS Rattus sp.  
XX PN WO9B15179-A1.  
XX PD 16-APR-1998.  
XX PF 08-OCT-1997; 97WO-US018145.  
XX PR 08-OCT-1996; 96US-0027981P.  
XX PA (UNIW ) UNIV WASHINGTON.  
XX PI Castillo G, Snow AD;  
XX DR WPI; 1998-240534/21.  
XX PT Use of laminin and fragments - for developing products for use in the  
PT diagnosis and treatment of amyloid disease, e.g. Alzheimer's disease or  
PT CJD.  
XX PS Claim 15; Page 94-97; 132pp; English.

This is the amino acid sequence of the rat laminin B2 chain. The primary object of the invention is to use laminin, laminin-derived protein fragments and/or laminin-derived polypeptides as potent inhibitors of amyloid formation, deposition, accumulation and/or persistence in Alzheimer's disease and other amyloidoses. The laminin products (see AAW50888-98) may include mammalian laminin A or A1 chain, laminin B1 or B2 chain, laminin A2 chain (merosin), laminin G1 chain, the globular repeats of the laminin A1 chain and the beta-amyloid binding domain of the laminin A chain. A claimed method for treating an amyloid disease comprises administering a polypeptide having a conformational similarity to a fragment of a laminin protein. A method for diagnosing an amyloid disease involves determining levels of laminin in a sample. Production of laminin or its fourth globular repeat in vivo provides a method for in vivo inhibition of beta-amyloid amyloidosis. The products and methods can be used for the diagnosis, prognosis, monitoring and treatment of amyloidoses such as Alzheimer's disease, Down's syndrome and hereditary cerebral haemorrhage with amyloidosis of the Dutch type (where the specific amyloid is the beta-amyloid protein), the amyloidosis associated with chronic inflammation, various forms of malignancy and Familial Mediterranean Fever (AA amyloid or inflammation-associated amyloidosis), the amyloidosis associated with multiple myeloma and other B-cell abnormalities (AL amyloid), the amyloidosis associated with type II diabetes (amylin or islet amyloid), the amyloidosis associated with prion diseases including Creutzfeldt-Jacob disease, Gerstmann-Strausler syndrome, kuru and animal scrapie (PrP amyloid), the amyloidosis associated with long-term haemodialysis and carpal tunnel syndrome (beta 2-microglobulin amyloid), the amyloidosis associated with senile cardiac amyloid and Familial Amyloidotic Polynuropathy (prealbumin or transthyretin amyloid), and the amyloidosis associated with endocrine tumours such as medullary carcinoma of the thyroid (variant of

CC procalcitonin)

XX SQ Sequence 1801 AA;

Query Match 29.4%; Score 60; DB 2; Length 1801;

Best Local Similarity 29.8%; Pred. No. 2.1e+02;

Matches 14; Conservative 5; Mismatches 8; Indels 20; Gaps 3;

QY 5 YQGKCHCHM-----GTHCHSSD-GPRGVIPERPC 32

DB 1113 FTGQCHCHAGFGGRTCTCSEQLHWDGFLQCRACDCDPRG-IDKPOC 1158

RESULT 14

ADBE0383

ID ADBE0383 standard; protein; 1801 AA.

XX AC ADBE0383;

XX DT 29-JAN-2004 (first entry)

XX DE Rat Protein P15800, SEQ ID NO 6292.

XX KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;

XX KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX OS Rattus norvegicus.

XX PN WO2003016475-A2.

XX PD 27-FEB-2003.

XX PF 14-AUG-2002; 2002WO-US025765.

XX PR 14-AUG-2001; 2001US-0312147P.

XX PR 01-NOV-2001; 2001US-0346382P.

XX PR 26-NOV-2001; 2001US-0333347P.

XX PA (GEHO) GEN HOSPITAL CORP.

XX PA (FARB) BAYER AG.

XX PI Woolf C, D'urso D, Befort K, Costigan M;

XX WPI; 2003-269312/26.

XX DR GENBANK; P15800.

XX PT New composition comprising two or more isolated polypeptides, useful for

XX PS preparing a medicament for treating pain in an animal.

XX Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat

XX or human polynucleotides or a polynucleotide which represents a fragment,

XX derivative or allelic variation of the nucleic acid sequence. Also

XX claimed are a vector comprising the novel polynucleotide, a host cell

XX comprising the vector, a method for identifying a nucleotide sequence

XX which is differentially regulated in an animal subjected to pain and a

XX kit to perform the method, an array, a method for identifying an agent

XX that increases or decreases the expression of the polynucleotide sequence

XX that is differentially expressed in neuronal tissue of a first animal

XX subjected to pain, a method for identifying a compound which regulates

XX the expression of a polynucleotide sequence which is differentially

XX expressed in an animal subjected to pain, a method for identifying a

XX compound that regulates the activity of one or more of the

XX polynucleotides, a method for producing a pharmaceutical composition, a

XX method for identifying a compound or small molecule that regulates the

XX activity in an animal of one or more of the polypeptides given in the

XX specification, a method for identifying a compound useful in treating

XX pain and a pharmaceutical composition comprising the one or more

XX polypeptides or their antibodies. The polynucleotide or the compound that

XX modulates its activity is useful for preparing a medicament for treating

XX pain (e.g. spinal segmental nerve injury (Chung), chronic constriction

XX injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. Gene

CC therapy). The sequence presented is a rat protein (shown in Table 2 of

CC the specification) which is differentially expressed during pain. Note:

CC The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic form directly from WIPO at

CC ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 1801 AA;

Query Match 29.4%; Score 60; DB 7; Length 1801;

Best Local Similarity 29.8%; Pred. No. 2.1e+02;

Matches 14; Conservative 5; Mismatches 8; Indels 20; Gaps 3;

QY 5 YQGKCHCHM-----GTHCHSSD-GPRGVIPERPC 32

DB 1113 FTGQCHCHAGFGGRTCTCSEQLHWDGFLQCRACDCDPRG-IDKPOC 1158

RESULT 15

AAU43863

ID AAU43863 standard; protein; 57 AA.

XX AC AAU43863;

XX DT 13-FEB-2002 (first entry)

XX DE Propionibacterium acnes immunogenic protein #4759.

XX KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;

XX KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;

XX KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;

XX KW dermatological; osteopathic; neuroprotectant.

XX OS Propionibacterium acnes.

XX PN WO200181581-A2.

XX PD 01-NOV-2001.

XX PF 20-APR-2001; 2001WO-US012865.

XX PR 21-APR-2000; 2000US-0199047P.

XX PR 02-JUN-2000; 2000US-0208841P.

XX PR 07-JUL-2000; 2000US-0216747P.

XX PA (CORI-) CORIXA CORP.

XX PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;

XX PI L'maisonneuve J, Zhang Y, Jen S, Carter D;

XX WPI; 2001-616774/71.

XX DR N-PSDB; AAS59521.

XX PT Propionibacterium acnes polypeptides and nucleic acids useful for

XX PT vaccinating against and diagnosing infections, especially useful for

XX PT treating acne vulgaris.

XX PS Example 1; SEQ ID NO 5058; 1069pp; English.

XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic

XX polypeptides. The proteins and their associated DNA sequences are used in

XX the treatment, prevention and diagnosis of medical conditions caused by

XX P. acnes. The disorders include SAPHO syndrome (synovitis, acne,

XX pustulosis, hypertosis and osteomyelitis) uveitis and endophthalmitis.

XX P. acnes is also involved in infections of bone, joints and the central

XX nervous system, however it is particularly involved in the inflammatory

XX lesions associated with acne vulgaris. A method for detecting the

XX presence or absence of P. acnes in a patient comprises contacting a

XX sample with a binding agent that binds to the proteins of the invention

XX and determining the amount of bound protein in the sample. The

XX polypeptides may be used as antigens in the production of antibodies

XX specific for P. acnes proteins. These antibodies can be used to

XX downregulate expression and activity of P. acnes polypeptides and

XX therefore treat P. acnes infections. The antibodies may also be used as

CC diagnostic agents for determining P. acnes presence, for example, by  
 CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for  
 CC this patent did not form part of the printed specification, but was  
 CC obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX  
 SQ Sequence 57 AA;

Query Match 28.9%; Score 59; DB 4; Length 57;  
 Best Local Similarity 40.0%; Pred. No. 9.1; Indels 0; Gaps 0;  
 Matches 10; Conservative 4; Mismatches 11;

Qy 9 CHCHMGTHCHSSDGRGVPEPRCP 33  
 ||:||:|:|:|:|:|:|:|:|:|  
 Db 3 CHGNLGTGPHADTGTGVSQPSRP 27

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Title: US-10-036-444-6

Perfect score: 204

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17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	204	100.0	33	US-10-036-444-6	Sequence 6, Appli
2	204	100.0	190	US-10-036-444-2	Sequence 2, Appli
3	204	100.0	190	US-10-036-259-4	Sequence 4, Appli
4	169.5	83.1	185	US-10-036-259-7	Sequence 7, Appli
5	62	30.4	145	US-10-437-963-200771	Sequence 200771,
6	61.5	30.1	636	US-09-796-753-100	Sequence 100, App
7	61.5	30.1	636	US-09-796-753-124	Sequence 124, App
8	61	29.9	201	US-10-425-115-264880	Sequence 264880,
9	60	29.4	201	US-10-696-259-6	Sequence 6, Appli
10	60	29.4	1799	US-03-845-583-6	Sequence 6, Appli
11	60	29.4	1801	US-09-938-275-8	Sequence 8, Appli
12	59	28.9	160	US-10-424-599-166699	Sequence 166699,
13	59	28.9	2813	US-09-886-900-2	Sequence 2, Appli

14	58.5	28.7	148	14	US-10-106-698-5317	Sequence 5317, Ap
15	58.5	28.7	1015	15	US-10-419-026-1	Sequence 1, Appli
16	58.5	28.7	2203	16	US-10-322-281-726	Sequence 726, App
17	58.5	28.7	2469	17	US-10-190-115-2	Sequence 2, Appli
18	58.5	28.7	2469	15	US-10-369-072-2	Sequence 2, Appli
19	58.5	28.7	2471	17	US-10-720-896A-12	Sequence 12, Appli
20	58	28.4	845	9	US-09-983-531A-6	Sequence 6, Appli
21	57.5	28.2	89	15	US-10-424-599-190841	Sequence 190841,
22	56.5	27.7	969	15	US-10-052-648A-34	Sequence 34, Appli
23	56.5	27.7	969	15	US-10-052-648A-35	Sequence 35, Appli
24	56	27.5	100	17	US-10-425-115-334473	Sequence 115759,
25	56	27.5	135	16	US-10-437-963-115759	Sequence 36099, A
26	56	27.5	239	16	US-10-767-701-36099	Sequence 272280,
27	55.5	27.2	125	15	US-10-424-599-272280	Sequence 358052,
28	55.5	27.2	128	17	US-10-425-115-358052	Sequence 9, Appli
29	55.5	27.2	198	16	US-10-696-259-9	Sequence 20, Appli
30	55.5	27.2	601	9	US-09-802-582-20	Sequence 20, Appli
31	55.5	27.2	601	14	US-10-365-227-20	Sequence 2, Appli
32	55.5	27.2	1140	14	US-10-092-390-2	Sequence 33, Appli
33	55.5	27.2	1140	15	US-10-052-648A-33	Sequence 1838, Ap
34	55.5	27.2	1140	16	US-10-408-765A-1838	Sequence 149149,
35	55	27.0	71	16	US-10-437-963-149149	Sequence 3183, Ap
36	54.5	26.7	580	14	US-10-128-714-3183	Sequence 8183, Ap
37	54.5	26.7	680	14	US-10-128-714-8183	Sequence 14, Appli
38	54.5	26.7	1535	14	US-10-189-971-14	Sequence 12, Appli
39	54.5	26.7	1570	14	US-10-189-971-12	Sequence 4, Appli
40	54.5	26.7	1593	14	US-10-189-971-4	Sequence 2, Appli
41	54.5	26.7	1628	14	US-10-189-971-2	Sequence 12, Appli
42	54.5	26.7	2710	13	US-10-153-273-12	Sequence 116, App
43	54	26.5	497	10	US-09-796-753-116	Sequence 302949,
44	54	26.5	698	17	US-10-425-115-302949	Sequence 4, Appli
45	54	26.5	928	15	US-10-052-648A-4	

#### ALIGNMENTS

#### RESULT 1

US-10-036-444-6  
; Sequence 6, Application US/10036444  
; Publication No: US20020142445A1  
; GENERAL INFORMATION:  
; APPLICANT: INNATE PHARMA S.A.S.  
; APPLICANT: UNIVERSITA DI GENOVA  
; TITLE OF INVENTION: "No. US20020142445A1e1 triggering receptor involved in natural  
; TITLE OF INVENTION: cytotoxicity mediated by human Natural Killer cells and  
; TITLE OF INVENTION: antibodies that identify the same"  
; FILE REFERENCE: SEQ-FR-1060  
; CURRENT APPLICATION NUMBER: US/10/036,444  
; CURRENT FILING DATE: 2002-01-07  
; PRIOR APPLICATION NUMBER: 09/440,514  
; PRIOR FILING DATE: 1999-11-15  
; PRIOR APPLICATION NUMBER: 09/456,199  
; PRIOR FILING DATE: 1999-12-07  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 33  
; TYPE: PRT  
; ORGANISM: Human NK cell  
US-10-036-444-6

Query Match 100.0%; Score 204; DB 13; Length 33;

Best Local Similarity 100.0%; Pred. No. 9.4e-17; Mismatches 0; Indels 0; Gaps 0;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 STVYQKCHCHMGTHCHSSDGRGVIPERCP 33

#### RESULT 2

US-10-036-444-2

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; Sequence 2, Application US/10036444
; Publication No. US20020142445A1
; GENERAL INFORMATION:
; APPLICANT: INNATE PHARMA S.A.S.
; TITLE OF INVENTION: "No. US20020142445A1 triggering receptor involved in natural
; TITLE OF INVENTION: cytotoxicity mediated by human Natural Killer cells and
; TITLE OF INVENTION: antibodies that identify the same"
; FILE REFERENCE: SEQ-PR-1060
; CURRENT APPLICATION NUMBER: US/10/036.444
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 09/440,514
; PRIOR FILING DATE: 1999-11-15
; PRIOR APPLICATION NUMBER: 09/456,199
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Human NK cell
US-10-036-444-2

Query Match      100.0%; Score 204; DB 13; Length 190;
Best Local Similarity 100.0%; Pred. No. 4.8e-16;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STVYQKCHCHMGTHCHSDGPRGVIPEPRCP 33
Db 158 STVYQKCHCHMGTHCHSDGPRGVIPEPRCP 190

RESULT 3
US-10-696-259-4
; Sequence 4, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-4

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Best Local Similarity 100.0%; Pred. No. 4.8e-16;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STVYQKCHCHMGTHCHSDGPRGVIPEPRCP 33
Db 158 STVYQKCHCHMGTHCHSDGPRGVIPEPRCP 190

RESULT 4
US-10-696-259-7
; Sequence 7, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-7

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Best Local Similarity 100.0%; Pred. No. 4.8e-16;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 158 STVYQKCHCHMGTHCHSDGPRGVIPEPRCP 190

RESULT 5
US-10-437-963-200771
; Sequence 200771, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 200771
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_96208C.1.pep
US-10-437-963-200771

Query Match      30.4%; Score 62; DB 16; Length 145;
Best Local Similarity 34.9%; Pred. No. 14;
Matches 15; Conservative 3; Mismatches 3; Indels 22; Gaps 3;

QY 12 HMGTHCHSDGPRGVI--PEP-----RCP 33
Db 36 HLAHCH-SDGPPGLACQPEPLPFSMSGVWTRARRSVRCP 77

RESULT 6
US-09-796-753-100
; Sequence 100, Application US/09796753
; Publication No. US20030027998A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean A.

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DB 411 CQCHHGATCHPQDGGSCVCIPGWTGPNC 437

## RESULT 8

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US-10-425-115-264880
; Sequence 264880, Application US/10425115
; Publication NO. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 264880
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_173179C.1.pep
US-10-425-115-264880

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US-09-845-583-6
; Sequence 6, Application US/09845583
; Patent No. US20020142954A1
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert
; APPLICANT: Brunken, William Joseph
; APPLICANT: Champlaud, Marie-France
; APPLICANT: Hunter, Dale
; TITLE OF INVENTION: LAMININ 15 AND US2S THEREOF
; FILE REFERENCE: 10287-056001
; CURRENT APPLICATION NUMBER: US/09/845,583
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/200,863
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1799
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-845-583-6

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;; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
;; FILE REFERENCE: 38-21(53223)B  
;; CURRENT APPLICATION NUMBER: US/10/424,599  
;; CURRENT FILING DATE: 2003-04-28  
;; NUMBER OF SEQ ID NOS: 285684  
;; SEQ ID NO 166699  
;; LENGTH: 160  
;; TYPE: PRT  
;; ORGANISM: Glycine max  
;; FEATURE:  
;; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_121544C.1.pcp  
US-10-424-599-166699

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Best Local Similarity 50.0%; Pred. No. 34;  
Matches 12; Conservative 2; Mismatches 6; Indels 4; Gaps 2;

QY 9 CHCHMG--TCHSSDGRGVIPEP 30  
DB 6 CHCSLGRAACHYNH--RRVIPSP 27

RESULT 13  
US-09-886-900-2  
; Sequence 2, Application US/09886900  
; Patent No. US20020137051A1  
; GENERAL INFORMATION:  
; APPLICANT: Venta, Patrick J  
; Yuzbasiyan-Gurkan, Vilma  
; Schall, William D  
; Brewer, George J  
; TITLE OF INVENTION: DNA ENCODING CANINE VON WILLEBRAND  
; FACTOR AND METHODS OF USE  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Harness, Dickey & Pierce, P.C.  
; STREET: 5445 Corporate Drive  
; CITY: Troy  
; STATE: Michigan  
; COUNTRY: USA  
; ZIP: 48098

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/886,900  
FILING DATE: 21-Jun-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/896,449  
FILING DATE: 18-JUL-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, DeAnn F.  
REFERENCE/DOCKET NUMBER: 2115-001226  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 248-641-1600  
TELEFAX: 248-641-0270  
TELEX: 287637

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2813 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-886-900-2

Query Match 28.9%; Score 59; DB 9; Length 2813;  
Best Local Similarity 30.6%; Pred. No. 5e+02;  
Matches 15; Conservative 4; Mismatches 10; Indels 20; Gaps 3;

QY 4 YYQK-----CHCHMG-TCHSSDG-----PRGVIPEPRC 32  
DB 7.0 YDGEIFQPEDIFSDHHTMCYCEDGFHCTTSGGLGSLLPNPVLSPPRC 758

RESULT 14  
US-10-106-698-5317  
; Sequence 5317, Application US/10106698  
; Publication No. US20030109690A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptid  
; FILE REFERENCE: PA00521  
; CURRENT APPLICATION NUMBER: US/10/106,698  
; CURRENT FILING DATE: 2002-03-27  
; PRIOR APPLICATION NUMBER: PCT/US00/26524  
; PRIOR FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: US 60/157,137  
; PRIOR FILING DATE: 1999-09-29  
; PRIOR APPLICATION NUMBER: US 60/163,280  
; PRIOR FILING DATE: 1999-11-03  
; NUMBER OF SEQ ID NOS: 8564  
; SOFTWARE: PatentIn Ver. 3.0  
; SEQ ID NO 5317  
; LENGTH: 148  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (18)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-10-106-698-5317

Query Match 28.7%; Score 58.5; DB 14; Length 148;  
Best Local Similarity 43.5%; Pred. No. 37;  
Matches 10; Conservative 2; Mismatches 8; Indels 3; Gaps 1;

QY 10 HCHMGTHCHSSDGRGVIPEPRC 32  
DB 83 HCHLGRCHGRPQREGL---PRC 102

RESULT 15  
US-10-419-026-1  
; Sequence 1, Application US/10419026  
; Publication No. US20040058443A1  
; GENERAL INFORMATION:  
; APPLICANT: Artavanis-Tsakonas, Spyridon  
; APPLICANT: Fortini, Mark  
; APPLICANT: Matsuno, Kenji  
; TITLE OF INVENTION: MANIPULATION OF NON-TERMINALLY DIFFERENTIATED CELLS USING THE  
; FILE REFERENCE: 10910-096  
; CURRENT APPLICATION NUMBER: US/10/419,026  
; CURRENT FILING DATE: 2003-04-18  
; PRIOR APPLICATION NUMBER: 08/537,210  
; PRIOR FILING DATE: 1995-09-29  
; PRIOR APPLICATION NUMBER: 09/113,824  
; PRIOR FILING DATE: 1998-07-10  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 1015  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-419-026-1

Query Match 28.7%; Score 58.5; DB 15; Length 1015;  
Best Local Similarity 42.3%; Pred. No. 2.2e+02;  
Matches 11; Conservative 3; Mismatches 11; Indels 1; Gaps 1;

QY 7 GKCHCHMGTHC-HSSDGRGVIPEPR 31

Wed Nov 17 05:46:44 2004

us-10-036-444-6.open.rapb

Page 6

Db 193 GQVKRKGEQCVHTASGPRCFCPSFR 218

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Job time : 31.4987 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 16, 2004, 19:04:36 ; Search time 9.27851 Seconds  
(without alignments)  
235.867 Million cell updates/sec

Title: US-10-036-444-6

Perfect score: 204

Sequence: 1 STVYQKCHCHMGTHCHSSDGRGVIPERCP 33

Scoring table: BLOSUM62

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Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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5: /cgn2\_6/ptodata/1/iaa/PTCUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	29.4	1799	4 US-09-845-583A-6	Sequence 6, Appli
2	59	28.9	2813	3 US-08-896-449A-2	Sequence 2, Appli
3	59	28.9	2813	3 US-09-132-652-2	Sequence 2, Appli
4	59	28.9	2813	4 US-09-886-900A-2	Sequence 2, Appli
5	59	28.9	2813	4 US-09-662-478C-2	Sequence 2, Appli
6	58.5	28.7	1015	1 US-08-537-210A-1	Sequence 1, Appli
7	58.5	28.7	1015	3 US-09-113-825-1	Sequence 1, Appli
8	58.5	28.7	2471	1 US-08-185-432-16	Sequence 16, Appli
9	58.5	28.7	2471	1 US-08-083-590A-19	Sequence 19, Appli
10	58.5	28.7	2471	3 US-08-532-384-19	Sequence 19, Appli
11	58.5	28.7	2471	4 US-08-899-232-1	Sequence 1, Appli
12	58.5	28.7	2471	4 US-09-121-457-1	Sequence 1, Appli
13	57	27.9	92	4 US-09-270-767-38503	Sequence 38503, A
14	57	27.9	92	4 US-09-270-767-53720	Sequence 53720, A
15	54.5	26.7	78	4 US-09-513-999C-6923	Sequence 6923, Ap
16	54.5	26.7	2710	2 US-08-568-459A-12	Sequence 12, Appli
17	54.5	26.7	2710	2 US-08-487-826B-12	Sequence 12, Appli
18	54.5	26.7	2710	3 US-09-210-288-12	Sequence 12, Appli
19	54.5	26.7	3060	2 US-08-487-826B-14	Sequence 14, Appli
20	52.5	25.7	577	2 US-07-728-215-29	Sequence 29, Appli
21	52.5	25.7	577	3 US-08-938-085A-29	Sequence 29, Appli
22	52.5	25.7	577	4 US-10-072-844-29	Sequence 29, Appli
23	52.5	25.7	577	4 US-10-072-838-29	Sequence 29, Appli
24	52.5	25.7	577	4 US-10-072-841A-29	Sequence 29, Appli
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26	52.5	25.7	799	1 US-08-054-077C-2	Sequence 2, Appli
27	52	25.5	278	3 US-09-724-864-52	Sequence 52, Appli

#### ALIGNMENTS

##### RESULT 1

US-09-845-583A-6  
; Sequence 6, Application US/09845583A  
; Patent No. 6635616  
; GENERAL INFORMATION:  
; APPLICANT: Burgeson, Robert  
; APPLICANT: Brunken, William Joseph  
; APPLICANT: Champlaud, Marie-France  
; APPLICANT: Hunter, Dale  
; TITLE OF INVENTION: LAMININ 15 AND USES THEREOF  
; FILE REFERENCE: 10287-056001  
; CURRENT APPLICATION NUMBER: US/09/845,583A  
; PRIOR FILING DATE: 2001-04-30  
; PRIOR APPLICATION NUMBER: US 60/200,863  
; PRIOR FILING DATE: 2000-05-01  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 1799  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-845-583A-6

Query Match 29.4%; Score 60; DB 4; Length 1799;  
Best Local Similarity 29.8%; Pred. No. 31;  
Matches 14; Conservative 5; Mismatches 8; Indels 20; Gaps 3;

QY 5 YQKCHCHM-----GTHCHSSD-GPRGVIPERPC 32  
DB 1111 FTGQCHCHAGFGGRTCSCQELYWCDPGLQCRACDCDPRG-IDKPC 1156

##### RESULT 2

US-08-896-449A-2  
; Sequence 2, Application US/08896449A  
; Patent No. 6040143  
; GENERAL INFORMATION:  
; APPLICANT: Venta, Patrick J  
; APPLICANT: Yuzbasiyan-Gurkan, Vilma  
; APPLICANT: Schall, William D  
; APPLICANT: Brewer, George J  
; TITLE OF INVENTION: DNA ENCODING CANINE VON WILLEBRAND  
; TITLE OF INVENTION: FACTOR AND METHODS OF USE  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.  
; STREET: 5445 Corporate Drive  
; CITY: Troy  
; STATE: Michigan  
; COUNTRY: USA

28 25.5 420 4 US-09-252-991A-27434 Sequence 27434, A  
29 25.5 470 4 US-09-252-991A-27804 Sequence 27804, A  
30 25.0 70 4 US-09-381-546-21 Sequence 21, Appl  
31 25.0 207 3 US-08-974-022-47 Sequence 47, Appl  
32 25.0 207 3 US-08-795-445A-47 Sequence 47, Appl  
33 25.0 207 3 US-08-795-447A-47 Sequence 47, Appl  
34 25.0 207 3 US-08-974-186-47 Sequence 47, Appl  
35 25.0 207 3 US-08-795-446B-47 Sequence 133, App  
36 25.0 207 3 US-08-706-945D-133 Sequence 47, Appl  
37 25.0 207 4 US-08-577-788C-47 Sequence 47, Appl  
38 25.0 325 1 US-08-292-549-2 Sequence 2, Appli  
39 25.0 325 3 US-09-042-785A-9 Sequence 9, Appli  
40 25.0 325 5 PCT-US91-02207-2 Sequence 2, Appli  
41 50.5 24.8 298 3 US-09-080-044-9 Sequence 9, Appli  
42 50.5 24.8 298 3 US-09-531-857A-9 Sequence 9, Appli  
43 50.5 24.8 771 4 US-09-252-991A-24401 Sequence 24401, A  
44 50 24.5 277 1 US-08-690-457-5 Sequence 5, Appli  
45 50 24.5 277 2 US-08-628-187-5 Sequence 5, Appli

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; ZIP: 48098
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/896,449A
; FILING DATE: 18-JUL-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, DeAnn F.
; REFERENCE/DOCKET NUMBER: 2115-001226
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 248-641-1600
; TELEFAX: 248-641-0270
; TELEX: 287637
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2813 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-896-449A-2

Query Match      28.9%; Score 59; DB 3; Length 2813;
Best Local Similarity 30.6%; Pred. No. 66;
Matches 15; Conservative 4; Mismatches 10; Indels 20; Gaps 3;

QY      4 YYOQK-----CHCHMG-THCHSSDG-----PRGVIPPRC 32
Db      710 YYDGEIQPEDIFSDHHTMTCYCEDGFHCTTSGGLGSLLENPVLSPPRC 758

RESULT 3
US-09-132-652-2
; Sequence 2, Application US/09132652
; Patent No. 6074832
; GENERAL INFORMATION:
; APPLICANT: Venta, Patrick J.
; APPLICANT: Yuzbasiyan-Gurkan, Vilma
; APPLICANT: Schall, William D.
; APPLICANT: Brewer, George J.
; APPLICANT: Duffendeck, John
; TITLE OF INVENTION: DNA ENCODING CANINE VON WILLEBRAND FACTOR AND METHODS
; FILE REFERENCE: 21158-001226CPB
; CURRENT APPLICATION NUMBER: US/09/132,652
; CURRENT FILING DATE: 1998-08-11
; EARLIER APPLICATION NUMBER: 08/896,449
; EARLIER FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2813
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-132-652-2

Query Match      28.9%; Score 59; DB 3; Length 2813;
Best Local Similarity 30.6%; Pred. No. 66;
Matches 15; Conservative 4; Mismatches 10; Indels 20; Gaps 3;

QY      4 YYOQK-----CHCHMG-THCHSSDG-----PRGVIPPRC 32
Db      710 YYDGEIQPEDIFSDHHTMTCYCEDGFHCTTSGGLGSLLENPVLSPPRC 758

RESULT 4
US-09-886-900A-2
; Sequence 2, Application US/09886900A
; Patent No. 6767707
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, Spyridon
```

```

; APPLICANT: Venta, Patrick J.
; APPLICANT: Brewer, George J.
; APPLICANT: Vilma, Yuzbasiyan-Gurkan
; APPLICANT: Schall, William D.
; TITLE OF INVENTION: DNA ENCODING CANINE VON WILLEBRAND FACTOR AND METHODS
; FILE REFERENCE: UMV-1226CPPCUS
; CURRENT APPLICATION NUMBER: US/09/886,900A
; CURRENT FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US/09/662,478C
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/132,652
; PRIOR FILING DATE: 1998-08-11
; PRIOR APPLICATION NUMBER: PCT/US99/18153
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2813
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-886-900A-2

Query Match      28.9%; Score 59; DB 4; Length 2813;
Best Local Similarity 30.6%; Pred. No. 66;
Matches 15; Conservative 4; Mismatches 10; Indels 20; Gaps 3;

QY      4 YYOQK-----CHCHMG-THCHSSDG-----PRGVIPPRC 32
Db      710 YYDGEIQPEDIFSDHHTMTCYCEDGFHCTTSGGLGSLLENPVLSPPRC 758

RESULT 5
US-09-662-478C-2
; Sequence 2, Application US/09662478C
; Patent No. 6780583
; GENERAL INFORMATION:
; APPLICANT: Venta, Patrick J.
; APPLICANT: Brewer, George J.
; APPLICANT: Vilma, Yuzbasiyan-Gurkan
; APPLICANT: Schall, William D.
; TITLE OF INVENTION: DNA ENCODING CANINE VON WILLEBRAND FACTOR AND METHODS
; FILE REFERENCE: UMV-1226CPPCUS
; CURRENT APPLICATION NUMBER: US/09/662,478C
; CURRENT FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/132,652
; PRIOR FILING DATE: 1998-08-11
; PRIOR APPLICATION NUMBER: PCT/US99/18153
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2813
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-662-478C-2

Query Match      28.9%; Score 59; DB 4; Length 2813;
Best Local Similarity 30.6%; Pred. No. 66;
Matches 15; Conservative 4; Mismatches 10; Indels 20; Gaps 3;

QY      4 YYOQK-----CHCHMG-THCHSSDG-----PRGVIPPRC 32
Db      710 YYDGEIQPEDIFSDHHTMTCYCEDGFHCTTSGGLGSLLENPVLSPPRC 758

RESULT 6
US-08-537-210A-1
; Sequence 1, Application US/08537210A
; Patent No. 5780300
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, Spyridon
```



RESULT 7 .  
US-09-113-825-1  
; Sequence 1, Application US/09113825  
; Patent No. 6149902  
; GENERAL INFORMATION:  
; APPLICANT: Artavanis-Tsakonas, Spyridon  
; APPLICANT: Fortini, Mark  
; APPLICANT: Matsuno, Kenji  
; TITLE OF INVENTION: MANIPULATION OF NON-TERMINALLY  
; TITLE OF INVENTION: DIFFERENTIATED CELLS USING THE NOTCH PATHWAY  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036/2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible

REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 7326-006

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2471 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-185-432-16

Query Match 28.7%; Score 58.5; DB 1; Length 2471;
Best Local Similarity 42.3%; Pred. No. 67;
Matches 11; Conservative 3; Mismatches 11; Indels 1; Gaps 1;

QY 7 GKCHCHMGTHC-HSSDGRGVPEPR 31
Db 1347 GQVKCRKGECVHTASGRFCFSPR 1372

RESULT 9
US-08-083-590A-19
; Sequence 19, Application US/08083590A
; Patent No. 5786158
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, S. et al.
; TITLE OF INVENTION: Therapeutic And Diagnostic Methods
; TITLE OF INVENTION: And Compositions Based On No. 5786158ch Proteins And
; TITLE OF INVENTION: Nucleic Acids
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/083,590A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/083,590
; FILING DATE: 25-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-015
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2471 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-083-590A-19

Query Match 28.7%; Score 58.5; DB 1; Length 2471;
Best Local Similarity 42.3%; Pred. No. 67;
Matches 11; Conservative 3; Mismatches 11; Indels 1; Gaps 1;

QY 7 GKCHCHMGTHC-HSSDGRGVPEPR 31
Db 1347 GQVKCRKGECVHTASGRFCFSPR 1372

RESULT 10
US-08-532-384-19
; Sequence 19, Application US/08532384
; Patent No. 6083904
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, S. et al.
; TITLE OF INVENTION: Therapeutic And Diagnostic Methods
; TITLE OF INVENTION: And Compositions Based On No. 6083904ch Proteins And
; TITLE OF INVENTION: Nucleic Acids
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/532,384
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/083,590
; FILING DATE: 25-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-015
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2471 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-532-384-19

Query Match 28.7%; Score 58.5; DB 3; Length 2471;
Best Local Similarity 42.3%; Pred. No. 67;
Matches 11; Conservative 3; Mismatches 11; Indels 1; Gaps 1;

QY 7 GKCHCHMGTHC-HSSDGRGVPEPR 31
Db 1347 GQVKCRKGECVHTASGRFCFSPR 1372

RESULT 11
US-08-899-232-1
; Sequence 1, Application US/08899232
; Patent No. 6436650
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Oi. Huilin
; TITLE OF INVENTION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON
; FILE REFERENCE: 7326-046
; CURRENT APPLICATION NUMBER: US/08/899,232
; CURRENT FILING DATE: 1997-07-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2471
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-899-232-1
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Query Match      28.7%; Score 58.5; DB 4; Length 2471;
Best Local Similarity 42.3%; Pred. No. 67;
Matches 11; Conservative 3; Mismatches 11; Indels 1; Gaps 1;

QY 7 GKCHCHMGTHC-HSSDGRGVIPR 31
Db 1347 GQVKCRKGEOCVHTASGRFCPSR 1372

RESULT 12
US-09-121-457-1
; Sequence 1, Application US/09121457
; Patent No. 6692919
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, S.
; APPLICANT: Qi, H.
; APPLICANT: Rand, M.
; TITLE OF INVENTION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON
; FILE REFERENCE: 7326-073
; CURRENT APPLICATION NUMBER: US/09/121,457
; CURRENT FILING DATE: 1998-07-23
; EARLIER APPLICATION NUMBER: 08/899,232
; EARLIER FILING DATE: 1997-07-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2471
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-121-457-1

Query Match      28.7%; Score 58.5; DB 4; Length 2471;
Best Local Similarity 42.3%; Pred. No. 67;
Matches 11; Conservative 3; Mismatches 11; Indels 1; Gaps 1;

QY 7 GKCHCHMGTHC-HSSDGRGVIPR 31
Db 1347 GQVKCRKGEOCVHTASGRFCPSR 1372

RESULT 13
US-09-270-767-38503
; Sequence 38503, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38503
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-38503

Query Match      27.9%; Score 57; DB 4; Length 92;
Best Local Similarity 41.2%; Pred. No. 3.7;
Matches 7; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 7 GKCHCHMGTHCHSSDGP 23
Db 27 GNCYCYLGSYCSRTFGP 43

RESULT 14
US-09-270-767-53720
; Sequence 53720, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
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; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 53720
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-53720

Query Match      27.9%; Score 57; DB 4; Length 92;
Best Local Similarity 41.2%; Pred. No. 3.7;
Matches 7; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 7 GKCHCHMGTHCHSSDGP 23
Db 27 GNCYCYLGSYCSRTFGP 43

RESULT 15
US-09-513-999C-6923
; Sequence 6923, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1998-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 6923
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-6923

Query Match      26.7%; Score 54.5; DB 4; Length 78;
Best Local Similarity 29.1%; Pred. No. 6.4;
Matches 16; Conservative 5; Mismatches 11; Indels 23; Gaps 4;

QY 2 TVVYO-----GKCHC-----HMGTGC-----HSSDGRGV-----IPRCP 33
Db 15 TTYVQHSQSPSCSPAHCPLRLTRHAGPLCLFTFSSNEAPRGLLWHPVPQLLCP 69

Search completed: November 16, 2004, 19:17:45
Job time : 10.2785 secs
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Result No.	Query		Score	Match	Length	DB	ID	Description
1	46.5	54.7	155	2	H97849	peptidoglycan-asso		
2	46.5	54.7	155	2	F71637	peptidoglycan-asso		
3	45	52.9	353	2	T01256	probable anthocyan		
4	43	50.6	305	2	T36261	hypothetical prote		
5	43	50.6	514	2	A49838	site-specific reco		
6	43	50.6	514	2	AD1988	fdxn element site-		
7	43	50.6	687	2	AD2347	ribonuclease E (im		
8	42	49.4	101	2	F75512	conserved hypothet		
9	42	49.4	372	1	S28296	hypothetical prote		
10	42	49.4	478	1	S60754	transcription fact		
11	42	49.4	486	1	TVHUEG	transforming prote		
12	42	49.4	535	2	F75159	hypothetical prote		
13	42	49.4	1317	2	F83310	conserved hypothet		
14	41.5	48.8	60	2	S68769	short neurotoxin -		
15	41	48.2	272	2	S36641	flagellar motor ap		
16	41	48.2	347	2	F71436	larnesyl-pyrophosp		
17	41	48.2	368	2	S67507	morphogen lefty pr		
18	41	48.2	517	2	C89840	conserved hypothet		
19	41	48.2	597	2	T08681	adenosylhomocystei		
20	41	48.2	788	2	AQ0786	secreted effector		
21	41	48.2	805	2	T24399	hypothetical prote		
22	40	47.1	196	2	H64968	acetyl CoA acetyl		
23	40	47.1	209	2	B83329	probable acyltrans		
24	40	47.1	316	2	E75566	probable repressor		
25	40	47.1	341	2	S46899	hypothetical prote		
26	40	47.1	341	2	B35769	CAMP response elem		
27	40	47.1	341	2	S03343	CAMP response elem		
28	40	47.1	349	2	D75419	proline dipeptidas		
29	40	47.1	396	2	E64049	cystathionine beta		

Query Match 54.7%; Score 46.5; DB 2; Length 155;  
Best Local Similarity 50.0%; Pred. No. 2.6;  
Matches 8; Conservative 5; Mismatches 2; Indels

QY 1 WWSQPPEIR-TLGGSC 15  
 Db 74 WLSKHPEVKVTVGGHC 89

RESULT 3  
 T01256  
 Probable anthocyanidin synthase [imported] - Arabidopsis thaliana  
 N;Alternate names: SRG1 protein homolog F16M14.17  
 C;Species: Arabidopsis thaliana (mouse-ear cress)  
 C;Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 09-Jul-2004  
 C;Accession: T01256; F04802  
 R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, July 1998  
 A;Description: Arabidopsis thaliana chromosome II BAC F16M14 genomic sequence.  
 A;Reference number: Z14213  
 A;Accession: T01256  
 A;Status: translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-353 <RCU>  
 A;Cross-references: UNIPROT:O80449; EMBL:AC003028; NID:G3335356; PID:G3335372  
 A;Experimental source: cultivar Columbia  
 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999  
 A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
 A;Reference number: A84420; MUID:20083487; PMID:10617197  
 A;Accession: F84802  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-353 <STO>  
 A;Cross-references: GB:AE002093; NID:G3335372; PIDN:AAC27173.1; GSPDB:GN00139  
 C;Genetics:  
 A;Map position: 2  
 A;Introns: 160/2; 271/3  
 C;Superfamily: 1-aminocyclopropane-1-carboxylate oxidase

Query Match 52.9%; Score 45; DB 2; Length 353;  
 Best Local Similarity 72.7%; Pred. No. 11;  
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WWSQPPEIRTL 11  
 Db 152 WSPQPKIREL 162

RESULT 4  
 T36261  
 Hypothetical protein SCE68.11 - Streptomyces coelicolor  
 C;Species: Streptomyces coelicolor  
 C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
 C;Accession: T36261  
 R;Murphy, L.; Harris, K.D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, June 1999  
 A;Reference number: Z21576  
 A;Accession: T36261  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-305 <MUR>  
 A;Cross-references: UNIPROT:Q9WX21; EMBL:AL079345; PIDN:CAB45347.1; GSPDB:GN00070; SCOED  
 A;Experimental source: strain A3(2)  
 C;Genetics:  
 A;Gene: SCOEDB:SCE68.11

Query Match 50.6%; Score 43; DB 2; Length 305;  
 Best Local Similarity 63.6%; Pred. No. 20;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WWSQPPEIRTL 11  
 Db 140 WVGPRPREVRTL 150

RESULT 5  
 A49838  
 site-specific recombinase XisF - Anabaena sp. (strain PCC 7120)  
 C;Species: Anabaena sp.  
 C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 15-Oct-1999  
 C;Accession: A49838  
 R;Carrasco, C.D.; Ramaswamy, K.S.; Ramasubramanian, T.S.; Golden, J.W. Genes Dev. 8, 74-83, 1994  
 A;Title: Anabaena xisF gene encodes a developmentally regulated site-specific recombinase  
 A;Reference number: A49838; MUID:94116860; PMID:8288129  
 A;Accession: A49838  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-514 <CAR>  
 A;Cross-references: GB:L23220; NID:G349678; PIDN:AAA16762.1; PID:G349679  
 C;Genetics:  
 A;Gene: xisF

Query Match 50.6%; Score 43; DB 2; Length 514;  
 Best Local Similarity 53.8%; Pred. No. 33;  
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 VSQPPEIRTLGGS 14  
 Db 414 VEEPPPEVKTLLRAS 426

RESULT 6  
 AF1988  
 fdxN element site-specific recombinase [imported] - Nostoc sp. (strain PCC 7120)  
 C;Species: Nostoc sp. PCC 7120  
 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
 C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
 C;Accession: AF1988  
 R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001  
 A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena  
 A;Reference number: AB1807; MUID:21595285; PMID:11759840  
 A;Accession: AF1988  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-514 <KUR>  
 A;Cross-references: UNIPROT:Q8WY3; GB:BA000019; PIDN:BAE73414.1; PID:G17130804; GSPDB:G  
 A;Experimental source: strain PCC 7120  
 C;Genetics:  
 A;Gene: xisF

Query Match 50.6%; Score 43; DB 2; Length 514;  
 Best Local Similarity 53.8%; Pred. No. 33;  
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 VSQPPEIRTLGGS 14  
 Db 414 VEEPPPEVKTLLRAS 426

RESULT 7  
 AD2347  
 ribonuclease E [imported] - Nostoc sp. (strain PCC 7120)  
 C;Species: Nostoc sp. PCC 7120  
 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
 C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
 C;Accession: AD2347  
 R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001  
 A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena  
 A;Reference number: AB1807; MUID:21595285; PMID:11759840  
 A;Accession: AD2347  
 A;Status: preliminary

```
A;Molecule type: DNA
A;Residues: 1-687 <KUR>
A;Cross-references: UNIPROT:Q8YP69; GB:BA000019; PIDN:BA076030.1; PID:gl17133467; GSPDB:C
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alr4331

Query Match      50.6%; Score 43; DB 2; Length 687;
Best Local Similarity 72.7%; Pred. No. 44;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VSQPPPIRTLE 12
Db 560 VSEPPPIRTVE 570
|:|||||:|
|:|||||:|

RESULT 8
G75512
conserved hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: G75512
R;White, O.; Eisen, J.A.; Heideberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zaleski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: G75512
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-101 <WHI>
A;Cross-references: UNIPROT:Q8YR23; GB:AB001908; GB:AE000513; NID:g6458174; PIDN:AAF1006
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR0492
A;Map position: 1

Query Match      49.4%; Score 42; DB 2; Length 101;
Best Local Similarity 41.9%; Pred. No. 9.4;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WVSQPPPIRTLE 12
Db 84 WLAEPQVSVLE 95
|:|||||:|
|:|||||:|

RESULT 9
S28296
hypothetical protein C40H1.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S28296
R;Berke, M.
submitted to the EMBL Data Library, December 1992
A;Reference number: S28296
A;Accession: S28296
A;Molecule type: DNA
A;Residues: 1-372 <BER>
A;Cross-references: UNIPROT:Q03571; EMBL:Z19154; NID:g6650; PID:g6651
C;Genetics:
A;Antons: 72/1; 109/2; 252/3; 324/3
C;Superfamily: Caenorhabditis elegans hypothetical protein C40H1.1, ribonucleoprotein re
F;59-139/Domain: ribonucleoprotein repeat homology <RRM2>

Query Match      49.4%; Score 42; DB 1; Length 372;
Best Local Similarity 61.9%; Pred. No. 35;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 VSQPPPIRTLEGS 14
Db 21 VSAPPEYKRLDGS 33
|:|||||:|
|:|||||:|
```

```
RESULT 10
S60754
transcription factor erg - chicken
C;Species: Gallus gallus (chicken)
C;Date: 27-Apr-1996 #sequence_revision 23-May-1997 #text_change 09-Jul-2004
C;Accession: S60754
R;Dhordain, P.; Dewitte, F.; Desbiers, X.; Stehelin, D.; Duterque-Coquilland, M.
Mech. Dev. 50, 17-28, 1995
A;Title: Mesodermal expression of the chicken erg gene associated with precartilaginous
A;Reference number: S60754; MUID:95329425; PMID:7605748
A;Accession: S60754
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-478 <DHO>
A;Cross-references: UNIPROT:Q90837; EMBL:X77159; NID:g790439; PIDN:CAA54404.1; PID:g790
C;Genetics:
A;Gene: erg
C;Superfamily: transcription factor erg; ets DNA-binding domain homology; ets RII regul
C;Keywords: DNA binding; phosphoprotein; proto-oncogene; transcription factor; transfer
F;119-193/Domain: ets RII regulatory region homology <ETR>
F;312-390/Domain: ets DNA-binding domain homology <ETS>

Query Match      49.4%; Score 42; DB 1; Length 478;
Best Local Similarity 46.7%; Pred. No. 45;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 WVSQPPPIRTLEGSC 15
Db 56 WLSQPPARVTIKMEC 70
|:|||||:|
|:|||||:|

RESULT 11
TVHUEG
transforming protein erg-3 - human
N;Contains: transforming protein erg-1; transforming protein erg-2
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1989 #sequence_revision 30-May-1997 #text_change 09-Jul-2004
C;Accession: A94294; A94178; I58410; A28041; A29515
R;Rao, V.N.; Papas, T.S.; Shyam, E.; Reddy, P.
Science 237, 635-639, 1987
A;Title: The erg gene: a human gene related to the ets oncogene.
A;Reference number: A94178; MUID:87317608; PMID:33476934
A;Accession: A94178
A;Molecule type: mRNA
A;Residues: 100-231,256-486 <REB>
A;Cross-references: UNIPROT:P11308; UNIPROT:Q16113; GB:M17254; NID:g182186; PIDN:AAA523
R;Reddy, E.S.P.; Rao, V.N.; Papas, T.S.
Proc. Natl. Acad. Sci. U.S.A. 84, 6131-6135, 1987
A;Title: The erg gene: a human gene related to the ets oncogene.
A;Reference number: A94178; MUID:87317608; PMID:33476934
A;Accession: A94178
A;Molecule type: mRNA
A;Residues: 100-231,256-486 <REB>
A;Cross-references: GB:M21535; NID:g182182; PIDN:AAA35811.1; PID:g182185
R;Prasad, D.D.; Rao, V.N.; Lee, L.; Reddy, E.S.
Oncogene 9, 669-673, 1994
A;Title: Differentially spliced erg-3 product functions as a transcriptional activator.
A;Reference number: I58410; MUID:94119611; PMID:8290279
A;Accession: I58410
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 230-259 <RES>
A;Cross-references: GB:S68130; NID:g544960; PIDN:AAB29724.1; PID:g544961
C;Genetics:
A;Gene: GDB:ERG
A;Cross-references: GDB:I19884; OMIM:165080
A;Map position: 21q22.2-21q22.2
C;Superfamily: transcription factor erg; ets DNA-binding domain homology; ets RII regul
C;Keywords: alternative splicing; DNA binding; nucleus; proto-oncogene; transcription f
F;1-231,256-486/Product: transforming protein erg-2 #status predicted <EG2>
F;100-231,256-486/Product: transforming protein erg-1 #status predicted <EG1>
F;128-200/Domain: ets RII regulatory region homology <ETR>
```

F;320-398/Domain: ets DNA-binding domain homology <ETS>

Query Match 49.4%; Score 42; DB 1; Length 486;

Best Local Similarity 46.7%; Pred. No. 46;

Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 WVSQPEIRTLGSC 15

Db 63 WLSQPPARVIRKMEC 77

RESULT 12

S75159 hypothetical protein sir1771 - *Synechocystis* sp. (strain PCC 6803)

C;Species: *Synechocystis* sp.

A;Variety: PCC 6803

C;Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004

C;Accession: S75159

R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.

O; K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda

DNA Res. 3, 109-136, 1996

A;Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*

s.

A;Reference number: S74322; MUID:97061201; PMID:8905231

A;Accession: S75159

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-535 <AN>

A;Cross-references: UNIPROT:P73052; EMBL:D90903; GB:AB001339; NID:G1652127; PIDN:BA11707

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 49.4%; Score 42; DB 2; Length 535;

Best Local Similarity 85.7%; Pred. No. 50;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WVSQPE 7

Db 203 WISQPE 209

RESULT 13

F83310 conserved hypothetical protein PA2684 [imported] - *Pseudomonas aeruginosa* (strain PA01)

C;Species: *Pseudomonas aeruginosa*

C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004

C;Accession: F83310

R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,

.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho

A;Reference number: A82950; MUID:20437337; PMID:10984043

A;Accession: F83310

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1317 <STO>

A;Cross-references: UNIPROT:Q910F4; GB:AE004696; GB:AE004091; NID:G99498750; PIDN:AG0607

A;Experimental source: strain PA01

C;Genetics:

A;Gene: PA2684

C;Superfamily: rhsF protein

Query Match 49.4%; Score 42; DB 2; Length 1317;

Best Local Similarity 50.0%; Pred. No. 1.2e+02;

Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WVSQPEIRTLGSC 14

Db 155 WAAVPAELQIQEGS 168

RESULT 14

S68769

short neurotoxin - black-banded coral snake

N;Alternate names: alpha-neurotoxin

C;Species: *Micrurus nigrocinctus*

C;Date: 25-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change 09-Jul-2004

C;Accession: S68769

R;Rosso, J.P.; Vargas-Rosso, O.; Gutierrez, J.M.; Rochat, H.; Bougis, P.E.

Eur. J. Biochem. 238, 231-239, 1996

A;Title: Characterization of alpha-neurotoxin and phospholipase A(2) activities from *Mic*

in from *Micrurus nigrocinctus nigrocinctus*.

A;Reference number: S68769; MUID:96248443; PMID:8665942

A;Accession: S68769

A;Molecule type: protein

A;Residues: 1-60 <ROS>

A;Cross-references: UNIPROT:P80548

A;Experimental source: *Micrurus nigrocinctus* (black-banded coral snake)

C;Superfamily: snake toxin

C;Keywords: neurotoxin; venom

F;3-22,17-39,41-52,53-58/Disulfide bonds: #status predicted

Query Match 48.8%; Score 41.5; DB 2; Length 60;

Best Local Similarity 64.3%; Pred. No. 6.8;

Matches 9; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

Qy 3 SQPPEIRTL-EGSC 15

Db 9 SQPPTIKTCEGQC 22

RESULT 15

S39641 flagellar motor apparatus homolog ytxD - *Bacillus subtilis*

C;Species: *Bacillus subtilis*

C;Date: 08-Jun-1994 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004

C;Accession: S39641; B70003

R;Grundv, F.J.; Waters, D.A.; Takova, T.Y.; Henkin, T.M.

Mol. Microbiol. 10, 259-271, 1993

A;Title: Identification of genes involved in utilization of acetate and acetoin in *Bacil*

A;Reference number: S39641; MUID:95020526; PMID:7934817

A;Accession: S39641

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-272 <GRU>

A;Cross-references: UNIPROT:P39063; GB:U17309; NID:G661173; PIDN:AAA68282.1; PID:G348048

R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter

C.; Bron, S.; Brulliet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho

A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Brington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A;Authors: Folger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler

iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.

A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauesl

Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Fohl, I.M.; Portetelle

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,

A;Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Terpetra, P.; Tognoni, A.; Tosato, V.; Uchiyama,

akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpetra, P.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K

T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamamoto, H.; Yamamoto, H.; Yamamoto, H.

A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Dauchin, A.

A;Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.

A;Reference number: A69580; MUID:98044033; PMID:9384377

A;Accession: B70003

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-272 <KUN>

A;Cross-references: GB:299119; GB:AL009126; NID:G2635411; PIDN:CAB14951.1; PID:G2635457

A;Experimental source: strain 168

C;Genetics:

A;Gene: ytxD

C;Superfamily: flagellar motor rotation protein

C;Keywords: transmembrane protein

Query Match 48.2%; Score 41; DB 2; Length 272;

Best Local Similarity 42.9%; Pred. No. 37;

Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;



Qy 1 WVSOPPEIRTEGS 14  
| | | : : | : |  
Db 255 WQXQPKQVTKGS 268

Search completed: November 16, 2004, 19:15:59  
Job time : 6.10345 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2004, 18:56:15 ; Search time 16.7507 Seconds  
(without alignments)  
515.240 Million cell updates/sec

Title: US-10-036-444-7  
Perfect score: 85  
Sequence: 1 WVSQPPERTLEGSC 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374546 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot 02:.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	76	89.4	176	1 NCT3 MACFA	P61483 macaca fasc
2	76	89.4	180	1 NCT3 MACMU	O8mj02 macaca mula
3	76	89.4	201	1 NCT3_HUMAN	O14931 homo sapien
4	76	89.4	201	1 NCT3_PANTR	P61484 pan troglod
5	62	72.9	192	1 NCT3 RAT	O8cfd9 rattus norv
6	49	57.6	2201	2 O86NN1	O86nn1 drosophila
7	49	57.6	2529	2 Q9VWC0	Q9vwc0 drosophila
8	48	56.5	1512	2 Q93HF2	Q93hf2 streptomyc
9	48	56.5	1517	2 O82K7	O82k7 streptomyc
10	47.5	55.9	155	2 Q7P9U5	Q7p9u5 rickettsia
11	46.5	54.7	155	2 Q9ZCH2	Q9zch2 rickettsia
12	46.5	54.7	155	2 Q92GC3	Q92gc3 rickettsia
13	46	54.1	236	2 Q9TCC7	Q9tcc7 nephroselm
14	46	54.1	397	2 O84QL3	O84ql3 cryza sativ
15	45	52.9	196	2 O8H8H6	O8h8h6 cryza sativ
16	45	52.9	353	2 O80449	O80449 arabidopsis
17	45	52.9	353	2 O8LCL0	O8lcl0 arabidopsis
18	44	51.8	304	2 Q73X58	Q73x58 mycobacteri
19	44	51.8	304	2 AAS04769	Aas04769 mycobacte
20	44	51.8	650	2 Q8FWS2	Q8fws2 brucella su
21	44	51.8	688	1 E0MD MOUSE	O54839 mus musculu
22	44	51.8	688	2 Q9JUL1	Q9jil1 mus musculu
23	44	51.8	707	2 Q8BN22	Q8bn22 mus musculu
24	43.5	51.2	280	2 Q706L3	Q706l3 pseudomonas
25	43.5	51.2	280	2 CAE92937	Caes92937 pseudomon
26	43.5	51.2	280	2 Q8TEF5	Q8tef5 homo sapien
27	43	50.6	305	2 Q9WX21	Q9wx21 streptomyc
28	43	50.6	456	2 Q9W6Z9	Q9w6z9 xenopus lae
29	43	50.6	474	2 Q9ADU2	Q9adu2 salmoneilla
30	43	50.6	485	2 Q6GNZ9	Q6gnz9 xenopus lae
31	43	50.6	485	2 Q9W700	Q9w700 xenopus lae

32	43	50.6	514	2	Q44111	Q44111 anabaena sp
33	43	50.6	514	2	Q8YVW3	Q8yvw3 anabaena sp
34	43	50.6	687	2	Q8YP69	Q8yp69 anabaena sp
35	43	50.6	692	1	E0MD_XENLA	P79944 xenopus lae
36	42	49.4	101	2	Q9RX23	Q9rx23 deinococcus
37	42	49.4	129	2	Q6ZSQ3	Q6zsq3 homo sapien
38	42	49.4	129	2	BAC86894	Bac86894 homo sapi
39	42	49.4	317	2	O6XXK5	O6xxk5 homo sapien
40	42	49.4	317	2	AAP41719	Aap41719 homo sapi
41	42	49.4	325	2	O6XXK4	O6xxk4 homo sapien
42	42	49.4	325	2	AAP41720	Aap41720 homo sapi
43	42	49.4	360	2	Q9D6W8	Q9d6w8 mus musculu
44	42	49.4	372	1	YLF1_CAEEL	Q03571 caenorhabdi
45	42	49.4	383	1	TRMU_PASMU	Q9c1a3 pasteurella

## ALIGNMENTS

## RESULT 1

ID	NCT3 MACFA	STANDARD;	PRT;	176 AA.
AC	P61483; Q95JB8;			
DT	05-JUL-2004 (Rel. 44, Created)			
DT	05-JUL-2004 (Rel. 44, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Natural cytotoxicity triggering receptor 3 precursor (Natural killer cell p30-related protein) (NKP30) (NK-p30).			
DE	cell p30-related protein) (NKP30) (NK-p30).			
GN	Name=NCR3;			
OS	Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;			
OC	Cercopithecoidea; Macaca.			
OX	NCBI_TaxID=9541;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Lymphoid;			
RA	Rizzi M., Biasoni R.;			
RT	"Non MHC specific natural cytotoxicity receptors (NCR) expressed in Macaca fascicularis lymphoid cells."			
RL	Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.			
CC	!- FUNCTION: Cytotoxicity activating receptor that may contribute to the increased efficiency of activated natural killer (NK) cells to mediate tumor cell lysis (By similarity).			
CC	!- SUBUNIT: Interacts with CD32 (By similarity).			
CC	!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).			
CC	!- SIMILARITY: Belongs to natural cytotoxicity receptor (NCR) family.			
CC	!- SIMILARITY: Contains 1 immunoglobulin-like domain.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	EMBL; AJ278389; CAC41081.1; --			
DR	HSP; F16410; I185.			
DR	InterPro; IPR003599; IG.			
DR	InterPro; IPR007110; IG-like.			
DR	Pfam; PF00047; IG; 1.			
DR	SMART; SM00409; IG; 1.			
DR	PROSITE; PS50835; IG LIKE; 1.			
KW	Glycoprotein; Immunoglobulin domain; Receptor; Signal; Transmembrane.			
FT	SIGNAL	1	18	Potential.
FT	CHAIN	19	176	Natural cytotoxicity triggering receptor
FT	DOMAIN	19	135	Extracellular (Potential).
FT	TRANSMEM	136	156	Potential.
FT	DOMAIN	157	176	Cytoplasmic (Potential).
FT	DOMAIN	19	126	IG-like.
FT	DISULFID	39	108	By similarity.

FT CARBOHYD 42 42 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 121 121 N-linked (GlcNAc...) (Potential).  
 SQ SEQUENCE 176 AA; 19251 MW; 97B2A3B625E4AD54 CRC64;

Query Match 89.4%; Score 76; DB 1; Length 176;  
 Best Local Similarity 100.0%; Pred. No. 7.8e-05; Indels 0; Gaps 0;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVSQPEIRTELEGS 14  
 DB 20 WVSQPEIRTELEGS 33

## RESULT 2

IDENT NCT3 MACMU STANDARD; PRT; 180 AA.  
 AC Q8MJ02; Q8MJ01; Q95JB8;  
 DT 05-JUL-2004 (Rel. 44, Created)  
 DT 05-JUL-2004 (Rel. 44, Last sequence update)  
 DT 01-OCT-2004 (Rel. 45, Last annotation update)  
 DE Natural cytotoxicity triggering receptor 3 precursor (Natural killer cell p30-related protein) (NKP30) (NK-p30).  
 GN Name=NCR3;  
 OS Macaca mulatta (Rhesus macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Macaca.  
 OX NCBI\_TaxID=9544;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4), AND VARIANT VAL-156.  
 RA LaBonte M.L., Miller J., Levin N.L.;  
 RT "Molecular cloning of rhesus monkey Nkp46 and Nkp30 and identification of Nkp46SD and Nkp30S.";  
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 4), AND VARIANT VAL-156.  
 RC TISSUE=Lymphoid;  
 RA Rizzi M., Biassoni R.;  
 RT "NCR express by macaca NK cells.";  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Cytotoxicity activating receptor that may contribute to the increased efficiency of activated natural killer (NK) cells to mediate tumor cell lysis (By similarity).  
 CC -!- SUBUNIT: Interacts with CD32 (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=4;  
 CC Name=1;  
 CC IsoId=Q8MJ02-1; Sequence=Displayed;  
 CC Note=No experimental confirmation available;  
 CC Name=2;  
 CC Note=No experimental confirmation available;  
 CC IsoId=Q8MJ02-2; Sequence=VSP\_010414;  
 CC Name=3;  
 CC Note=No experimental confirmation available;  
 CC IsoId=Q8MJ02-3; Sequence=VSP\_010415, VSP\_010416;  
 CC Note=No experimental confirmation available;  
 CC Name=4;  
 CC IsoId=Q8MJ02-4; Sequence=VSP\_010417;  
 CC Note=No experimental confirmation available;  
 CC -!- SIMILARITY: Belongs to natural cytotoxicity receptor (NCR) family.  
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.

-----  
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 CC -----  
 DR EMBL; AY035214; AAK63116.1; -;  
 DR EMBL; AY035215; AAK63117.1; -;  
 DR EMBL; AY035216; AAK63118.1; -;

DR EMBL; AY035217; AAK63119.1; -;  
 DR EMBL; AJ554301; CAD86942.1; -;  
 DR HSSP; P16410; 1185.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00409; Ig; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Alternative splicing; Glycoprotein; Immunoglobulin domain; Polymorphism; Receptor; Signal; Transmembrane.  
 FT SIGNAL 1 18 Potential.  
 FT CHAIN 19 180 Natural cytotoxicity triggering receptor 3.  
 FT DOMAIN 19 133 Extracellular (Potential).  
 FT TRANSMEM 134 154 Potential.  
 FT DOMAIN 155 180 Cytoplasmic (Potential).  
 FT DOMAIN 19 126 Ig-like.  
 FT DISULFID 39 108 By similarity.  
 FT CARBOHYD 42 42 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 121 121 N-linked (GlcNAc...) (Potential).  
 FT VARSPLIC 66 90 Missing (in isoform 2).  
 FT VARSPLIC 112 115 VLGL -> NILS (in isoform 3).  
 FT VARSPLIC 116 180 Missing (in isoform 3).  
 FT VARSPLIC 177 180 Missing (in isoform 4).  
 FT VARIANT 156 156 Missing (in isoform 4).  
 SQ SEQUENCE 180 AA; 19639 MW; 5C2DF53487B2A3B6 CRC64;  
 M -> V.

Query Match 89.4%; Score 76; DB 1; Length 180;  
 Best Local Similarity 100.0%; Pred. No. 8e-05; Indels 0; Gaps 0;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVSQPEIRTELEGS 14  
 DB 20 WVSQPEIRTELEGS 33

## RESULT 3

IDENT NCT3 HUMAN STANDARD; PRT; 201 AA.  
 AC O14931; O14930; O14932; O95667; O95668; O95669;  
 DT 05-JUL-2004 (Rel. 44, Created)  
 DT 05-JUL-2004 (Rel. 44, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Natural cytotoxicity triggering receptor 3 precursor (Natural killer cell p30-related protein) (NKP30) (NK-p30).  
 GN Name=NCR3; Synonyms=IC7;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 2), TISSUE SPECIFICITY, INTERACTION WITH CD32, AND FUNCTION.  
 RC TISSUE=Lymphoid;  
 RX PubMed=10562324;  
 RA Pende D., Parolini S., Pessino A., Sivori S., Augugliaro R., Morelli L., Marcenaro E., Accame L., Malaspina A., Biassoni R., Bottino C., Moretta L., Moretta A.;  
 RT "Identification and molecular characterization of NKP30, a novel triggering receptor involved in natural cytotoxicity mediated by human natural killer cells.";  
 RL J. Exp. Med. 190:1505-1516(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 2), TISSUE SPECIFICITY, AND INTERACTION WITH CD32.  
 RC TISSUE=Peripheral blood;  
 RA Sato M., Yabe T., Ohashi J., Tsuchiya N., Hanaoka K., Tokunaga K., Juji T.;  
 RT "Identification of two novel single nucleotide polymorphisms in the

```

CC Name=5; Synonyms=IC7f;
CC IsoId=014931-5; Sequence=VSP_010411, VSP_010413;
CC Note=No experimental confirmation available;
CC Name=6; Synonyms=IC7d;
CC IsoId=014931-6; Sequence=VSP_010412;
CC Note=No experimental confirmation available;
CC TISSUE SPECIFICITY: Selectively expressed by all resting and
CC activated NK cells and weakly expressed in spleen.
CC -! SIMILARITY: Belongs to natural cytotoxicity receptor (NCR) family.
CC -! SIMILARITY: Contains 1 immunoglobulin-like domain.
CC
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CC
CC EMBL; AJ223153; CAB54004.1; -
CC EMBL; AB055881; BAB78472.1; -
CC EMBL; Y14768; CAA75063.1; -
CC EMBL; Y14768; CAA75064.1; -
CC EMBL; Y14768; CAA75065.1; -
CC EMBL; Y14768; CAA75066.1; -
CC EMBL; Y14768; CAA75067.1; -
CC EMBL; Y14768; CAA75068.1; -
CC EMBL; AF031136; AAB86578.1; -
CC EMBL; AF031137; AAB86579.1; -
CC EMBL; AF031138; AAB86580.1; -
CC EMBL; AF129756; AAD18088.1; -
CC EMBL; AP000505; BAB63393.1; -
CC EMBL; BC052582; AAH52582.1; -
CC Genew; HGNC:19077; NCR3.
CC GO; GO:0006955; P:immune response; NAS.
CC GO; GO:0006954; P:inflammatory response; NAS.
CC InterPro; IPR003599; IG.
CC Pfam; PF00047; IG-like.
CC SMART; SM00409; IG; 1.
CC PROSITE; PS50835; IG LIKE; 1.
CC Alternative splicing; Glycoprotein; Immunoglobulin domain; Receptor;
CC Signal; Transmembrane
CC SIGNAL 1 18
CC CHAIN 19 201
CC
CC Potential.
CC Natural cytotoxicity triggering receptor
CC 3.
CC Extracellular (Potential).
CC Potential.
CC Cytoplasmic (Potential).
CC IG-like.
CC By similarity.
CC N-linked (GlcNAc.. ) (Potential).
CC N-linked (GlcNAc.. ) (Potential).
CC Missing (in isoform 4, isoform 5 and
CC isoform 6).
CC /FTID=VSP_010411.
CC CLTWKPRRLPAVVPAPLPCCGSSAHLPPVPGG -> Y
CC AKSTLSGFPOL (in isoform 3 and isoform 6).
CC /FTID=VSP_010412.
CC LTWKPRRLPAVVPAPLPCCGSSAHLPPVPGG -> HC
CC HMGTHCHSSDGRGVIPEPRCP (in isoform 2 and
CC isoform 5).
CC /FTID=VSP_010413.
CC /FTID=VSP_010414.
CC
CC SEQUENCE 201 AA; 21593 MW; 2855AE4D6902D429 CRC64;
CC
CC Query Match 89.4%; Score 76; DB 1; Length 201;
CC Best Local Similarity 100.0%; Pred. No. 9e-05;
CC Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 1 WVSOPPEIRTLUEGS 14
CC DB 20 WVSOPPEIRTLUEGS 33

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RL Genome Res. 14:631-639(2004).
CC -!- FUNCTION: Cytotoxicity activating receptor that may contribute to
CC the increased efficiency of activated natural killer (NK) cells to
CC mediate tumor cell lysis (By similarity).
CC -!- SUBUNIT: Interacts with CD32 (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -!- SIMILARITY: Belongs to natural cytotoxicity receptor (NCR) family.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC -----
DR EMBL; AJ430418; CAD23066.1; -.
DR EMBL; AJ430419; CAD23067.2; -.
DR EMBL; AJ430420; CAD23067.2; JOINED.
DR EMBL; AY273824; AAP13457.1; -.
DR EMBL; BX883046; CAB84000.1; -.
DR RSP; P09793; IDQT.
DR RGD; 727881; 1C7.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; IG_1.
DR PROSITE; PS00835; IG-LIKE; 1.
KW Glycoprotein; Immunoglobulin domain; Polymorphism; Receptor; Signal;
KW Transmembrane.
FT SIGNAL 1 18 Potential.
FT CHAIN 19 192 Natural cytotoxicity triggering receptor
FT FT
FT DOMAIN 19 147 Extracellular (Potential).
FT TRANSMEM 148 168 Potential.
FT DOMAIN 169 192 Cytoplasmic (Potential).
FT DOMAIN 19 126 Ig-like.
FT DISULFID 39 108 By similarity.
FT VARIANT 7 7 I -> V.
FT VARIANT 19 19 I -> V.
FT VARIANT 82 82 A -> V.
FT VARIANT 138 138 A -> T.
FT CONFLICT 135 135 A -> V (in Ref. 2).
SQ SEQUENCE 192 AA; 20470 MW; 7FC84FB252D22377 CRC64;

Query Match 72.98; Score 62; DB 1; Length 192;
Best Local Similarity 78.68; Pred. No. 0.023; Indels 0; Gaps 0;
Matches 11; Conservative 1; Mismatches 2;

Qy 1 WVSQPPPIRTLEGS 14
Db 20 WVSQPPPIRTLEGS 33

RESULT 6
Q86NN1 PRELIMINARY; PRT; 2201 AA.
AC Q86NN1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE GH07949p (Fragment).
GN Name=CG11936; ORFNames=CG32529;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
R1 REINERT M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
R2 Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
R3 Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
R4 Reinert M., Remington K., Saunders R.D., Scheeler F., Shen H.,
R5 Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
R6 Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
R7 Svirskas R., Tector C., Turner C., Turner E., Wang A.H., Wang X.,
R8 Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissbach J.,

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RA Campe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BT004503; AAO42667.1; -.
DR FlyBase; FBgn0052529; CG32529.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001025; BAH.
DR Pfam; PF01426; BAH; 1.
DR SMART; SM00439; BAH; 1.
FT NON_TER 1
SQ SEQUENCE 2201 AA; 237099 MW; 10303133A8B4864B CRC64;

Query Match 57.68; Score 49; DB 2; Length 2201;
Best Local Similarity 81.88; Pred. No. 54;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 QPPEIRTLLEGS 14
Db 340 QPPEIRTLLEGS 350

RESULT 7
Q9VWC0 PRELIMINARY; PRT; 2529 AA.
AC Q9VWC0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CG32529-PA.
GN ORFNames=CG32529;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
R1 REINERT M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
R2 Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
R3 Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
R4 Reinert M., Remington K., Saunders R.D., Scheeler F., Shen H.,
R5 Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
R6 Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
R7 Svirskas R., Tector C., Turner C., Turner E., Wang A.H., Wang X.,
R8 Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissbach J.,

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RA Ikeda H., Ithikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermitilis.";
RL Nat. Biotechnol. 21:526-531(2003).
DR EMBL: AP005049; BAC74895.1; -.
DR GO: GO:0048037; F:cofactor binding; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR GO: GO:0006633; P:fatty acid biosynthesis; IEA.
DR GO: GO:0008152; P:metabolism; IEA.
DR InterPro: IPR003081; ACP like.
DR InterPro: IPR001227; AC transferase.
DR InterPro: IPR002194; Chaperonin_TCP.1.
DR InterPro: IPR000794; Ketoacyl synth.
DR InterPro: IPR008268; Peptid_S16_AS.
DR InterPro: IPR006163; Pp_bind.
DR Pfam: PF00698; Acyl_transf 1; 1.
DR Pfam: PF0109; ketoacyl-synt; 1.
DR Pfam: PF02801; Ketoacyl-synt C; 1.
DR Pfam: PF0550; pp-binding; 1.
DR PROSITE: PS00075; ACP DOMAIN; 1.
DR PROSITE: PS00605; E_KETOACYL_SYNTHASE; 1.
DR PROSITE: PS01045; LON_SER; UNKNOWN 1.
DR PROSITE: PS00995; TCPI_3; UNKNOWN 1.
KW Complete proteome; Transferase.
SQ SEQUENCE 1517 AA; 164167 MW; 43B0D4C75D48E962 CRC64;

Query Match 56.5%; Score 48; DB 2; Length 1517;
Best Local Similarity 61.5%; Pred.No.55;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 WVSQPPPIRTLEG 13
DB 944 WVEQPPTARTVAG 956

RESULT 10
Q7P9U5 PRELIMINARY; PRT; 155 AA.
AC Q7P9U5
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Peptidoglycan-associated lipoprotein precursor.
GN Name=rsib_orf.907;
OS Rickettsia sibirica.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=35793;
RN [1]
RP SEQUENCE FROM N.A.
RA Malek J.A., Ereneeva M.E., Dasch G.A.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the ompA family.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: AABW01000001; EAA26095.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.
DR InterPro: IPR006664; Bac_OmpA.
DR InterPro: IPR006665; OmpA/MotB.
DR Pfam: PF00651; OmpA; 1.
DR PRINTS; PR01021; OMPADOMAIN.
DR ProDom: PD000930; OmpA/MotB; 1.
DR Lipoprotein.
SQ SEQUENCE 155 AA; 17419 MW; 852EB9DC39B4C1E0 CRC64;

Query Match 55.9%; Score 47.5; DB 2; Length 155;
Best Local Similarity 50.0%; Pred.No.6.2;
Matches 8; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 1 WVSQPPPIR-TLEGSC 15

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 16, 2004, 17:12:10 ; Search time 15.9549 Seconds  
(without alignments)  
337.259 Million cell updates/sec

Title: US-10-036-444-7

Perfect score: 85

Sequence: 1 WVSQPEIRLBGSC 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A Geneseqp\_23Sep04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	100.0	15	4	Aae02774 Human Nkp
2	85	100.0	15	8	Adq30927 Human Nkp
3	76	89.4	120	4	Aae02771 Human Nkp
4	76	89.4	120	8	Adq30924 Human Nkp
5	76	89.4	135	5	Aae19109 Human Nkp
6	76	89.4	177	2	Aay06402 Human B-C
7	76	89.4	190	2	Aay06401 Human B-C
8	76	89.4	190	4	Aae02769 Human Nkp
9	76	89.4	190	8	Ado19810 Human PRO
10	76	89.4	190	8	Adq30923 Human Nkp
11	76	89.4	201	2	Aay06403 Human B-C
12	76	89.4	369	5	Aae19110 Human Nkp
13	66	77.6	382	8	Adp48750 Human Nkp
14	49	57.6	1289	4	Abb70840 Drosophila
15	45.5	53.5	83	8	Abos8908 Human gen
16	45	52.9	164	3	Aag27977 Human con
17	45	52.9	301	3	Aag43485 Arabidops
18	45	52.9	353	3	Aag43484 Arabidops
19	45	52.9	353	5	Abb92033 Herbicida
20	45	52.9	380	3	Aag43483 Arabidops
21	44	51.8	185	4	Abg23939 Mouse hum
22	44	51.8	688	3	Aay57393 Mouse ner
23	43.5	51.2	202	8	Adf69309 Human lun
24	43.5	51.2	211	8	Adf69308 Human lun
25	43	50.6	74	4	Aam88325 Human imm

26	43	50.6	276	4	ABG07919 Novel hum
27	43	50.6	303	8	ADP29234 Human sec
28	43	50.6	514	5	ABJ10466 XisF reco
29	42	49.4	63	5	ABP02197 Human ORF
30	42	49.4	134	3	AAQ01336 Human sec
31	42	49.4	383	6	ABU39323 Protein e
32	42	49.4	451	2	AAU01520 Chicken C
33	42	49.4	459	6	ABP97695 Amino aci
34	42	49.4	462	5	AAU75313 Human Brg
35	42	49.4	462	6	ABU03476 Angiogene
36	42	49.4	462	6	ABU56566 Lung canc
37	42	49.4	462	7	ABD75275 Prostate
38	42	49.4	478	2	AAU01521 Chicken c
39	42	49.4	1128	7	ABO82286 Pseudomon
40	42	49.4	1317	4	AAU33622 Pseudomon
41	42	49.4	1317	6	ABU15571 Protein e
42	41.5	48.8	116	5	ABP42291 Human ova
43	41	48.2	87	5	ABP33534 Human ORF
44	41	48.2	137	5	AAU80378 Human DOP
45	41	48.2	149	4	ABG02616 Novel hum

ALIGNMENTS

RESULT 1

AAE02774

ID AAE02774 standard; peptide; 15 AA.

XX

AC AAE02774;

XX

DT 06-AUG-2001 (first entry)

XX

DE Human Nkp30 receptor immunogenic peptide for antiserum production.

XX

KW Human; Nkp30 receptor; natural killer cell; cytostatic; antimicrobial;  
melanoma; hepatocarcinoma; lung adenocarcinoma; viral infection; tumour;  
immunopressant; antiviral; drug; grafting enhancement; leukaemia;  
therapy.

XX

OS Homo sapiens.

XX

PN WO200136630-A2.

XX

PD 25-MAY-2001.

XX

PF 15-NOV-2000; 2000WO-EP011697.

XX

PR 15-NOV-1999; 99CA-02288307.

XX

PR 15-NOV-1999; 99US-00440514.

XX

PA (INNA-) INNATE PHARMA SAS.

XX

PI (UYGE-) UNIV GENOVA.

XX

PI Moretta A, Bottino C, Biassoni R;

XX

WPI; 2001-329221/34.

XX

XX NK cells, comprises the amino acid sequences of the Nkp30 molecule.

XX

PS Claim 1; Page 33; 83pp; English.

XX

XX The invention relates to human Nkp30 receptor and its corresponding cDNA

CC molecule which is involved in natural cytotoxicity mediated by natural

CC killer (NK) cells and antibodies that identify the same. Nkp30 receptor

CC is a member of immunoglobulin super family (Ig-SF). Nkp30 is selectively

CC expressed on the surface of human mature NK cells. Nkp30 and its cDNA are

CC useful for detecting and/or quantifying the presence of NK cells in a

CC biological sample. The invention also provide kits for detecting and/or

CC quantifying the presence of NK cells, for the selective removal of NK

CC cells from a biological sample, for the positive and selective

CC purification of NK cells from a biological sample and for the in vitro



CC enhancement, graft versus host (GvH) inhibition, stimulation of graft  
CC versus tumour (GvT) and especially graft versus leukaemia (GvL), and for  
CC the prevention, palliation and/or therapy of solid or liquid tumours,  
CC such as melanoma, hepatocarcinoma and lung adenocarcinoma, and/or  
CC microorganism, notably viral infection. NKp30 antibodies are useful for  
CC identifying NKp30 natural ligands and allow assessment of the level of  
CC surface NKp30 ligand expressed on an NK-susceptible target cell and the  
CC comparison of this level to the standard physiological one. Hence NKp30  
CC antibodies are useful in the diagnosis of tumours or of infection. The  
CC present sequence is the extracellular region of human NKp30 receptor  
XX  
XX  
SQ Sequence 120 AA;

Query Match 89.4%; Score 76; DB 4; Length 120;  
Best Local Similarity 100.0%; Pred. No. 0.00026; Mismatches 0; Indels 0; Gaps 0;  
Matches 14; Conservative 0;

Qy 1 WVSQPPEIRLTLEGS 14  
| | | | | | | | | | | | | |  
Db 2 WVSQPPEIRLTLEGS 15

RESULT 4  
ADQ30924  
ID ADQ30924 standard; protein; 120 AA.  
XX  
AC ADQ30924;  
XX  
DT 23-SEP-2004 (first entry)  
XX  
DE Human NKp30 extracellular region.  
XX  
KW Natural killer cell; NK cell; NKp30; cytostatic; antimicrobial.  
XX  
OS Homo sapiens.  
XX  
PN WO2004056392-A1.  
XX  
PD 08-JUL-2004.  
XX  
PF 22-DEC-2003; 2003WO-EP014716.  
XX  
PR 23-DEC-2002; 2002US-0435344P.  
XX  
PA (INNA-) INNATE PHARMA.  
XX  
PI Romagne F, Andre P;  
XX  
WP1; 2004-507595/48.

XX Pharmaceutical compositions that stimulate proliferation of natural  
PT killer cells useful for therapy of melanoma, chronic myeloid, and  
PT leukemia, comprise an anti-natural killer cell receptor antibody and  
PT interleukins.  
XX  
PS Claim 3; SEQ ID NO 2; 35pp; English.  
XX  
CC The present sequence is that of the extracellular region of human NKp30  
CC ADQ30923, a 190 amino acid polypeptide that is selectively expressed by  
CC natural killer (NK) cells, and particularly by mature NK cells. Claimed  
CC pharmaceutical compositions that have a stimulating effect on the  
CC proliferation of NK cells comprise an antibody such as an anti-NKp30  
CC antibody or anti-NKp46 antibody or its immuno-reactive fragment and a  
CC cytokine selected from interleukin-2 (IL2), IL12, IL15 and IL21, the  
CC antibody(ies) and cytokine(s) being administered together or separately  
CC to a subject. The anti-NKp30 antibody is an isolated antibody or its  
CC antigen-binding fragment which specifically binds to NKp30 or to a  
CC fragment, including the extracellular region, of NKp30. The  
CC pharmaceutical compositions, when used for daily subcutaneous injection,  
CC comprising from 1 mg to 100 mg/Kg (body weight) of antibody(ies), and  
CC lower than 1 million units/square meters/day of cytokine(s), are useful  
CC for the prevention, palliation and therapy of e.g. melanoma, chronic  
CC myeloid leukaemia, acute myeloid leukaemia, lymphoma, multiple myeloma,

CC hepatocarcinoma, lung adenocarcinoma, neuroblastoma and for antimicrobial  
CC prevention, palliation and therapy (claimed).  
XX  
SQ Sequence 120 AA;

Query Match 89.4%; Score 76; DB 8; Length 120;  
Best Local Similarity 100.0%; Pred. No. 0.00026; Mismatches 0; Indels 0; Gaps 0;  
Matches 14; Conservative 0;

Qy 1 WVSQPPEIRLTLEGS 14  
| | | | | | | | | | | | | |  
Db 2 WVSQPPEIRLTLEGS 15

RESULT 5  
AAE19109  
ID AAE19109 standard; protein; 135 AA.  
XX  
AC AAE19109;  
XX  
DT 21-MAY-2002 (first entry)  
XX  
DE Human NKp30 protein.

XX Human; natural killer cell activating protein; NKp46; therapy; virucide;  
KW viral infection; natural killer cell; NK; NKp44; imaging agent; cancer;  
KW detection; carcinoma; melanoma; lymphoma; sarcoma; cytostatic; NKp30.  
XX  
OS Homo sapiens.  
XX  
PN WO200208287-A2.  
XX  
PD 31-JAN-2002.  
XX  
PF 19-JUL-2001; 2001WO-IL000664.  
XX  
PR 20-JUL-2000; 2000IL-00137419.  
XX  
PA (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
PA (UYNE ) UNIV BEN-GURION NEGEV.  
XX  
PI Mandelboim O, Porgador A;  
XX  
XX  
DR WP1; 2002-195870/25.  
DR N-PSDB; AAD30466.

XX New targeting complex capable of targeting an active substance to a  
PT target cell, comprising a target recognition segment and an active  
PT segment, useful for treating pathologies associated with viral infections  
PT or cancer.

XX Example 1; Page 108; 113pp; English.  
XX  
CC The invention relates to compositions and methods for the treatment and  
CC detection of a variety of viral infections, by using complex agents  
CC comprising the natural killer (NK) cells activating proteins, NKp46 and  
CC NKp44 and functional fragments thereof, linked to therapeutic or imaging  
CC agents. The complex is useful for treating pathologies associated with  
CC viral infections (e.g. infections caused by influenza virus, HIV, Epstein  
CC-Barr virus, cytomegalovirus, vaccinia virus, ECMV, MVM or herpes virus)  
CC and cancer (e.g. carcinomas, melanomas, lymphomas and sarcomas), and for  
CC the imaging and monitoring of cancer. The complex may also be used to  
CC detect the presence of abnormal cells in a sample. The antibodies can be  
CC used to qualitatively or quantitatively detect the ligand for the  
CC complex. The present sequence is human NKp30 protein

XX  
SQ Sequence 135 AA;

Query Match 89.4%; Score 76; DB 5; Length 135;  
Best Local Similarity 100.0%; Pred. No. 0.00029; Mismatches 0; Indels 0; Gaps 0;  
Matches 14; Conservative 0;

Qy 1 WVSQPPEIRLTLEGS 14  
| | | | | | | | | | | | | |  
Db 2 WVSQPPEIRLTLEGS 15

Db 20 WVSQPPPIRTLEGS 33  
 RESULT 6  
 AAY06402  
 ID AAY06402 standard; protein; 177 AA.  
 AC AAY06402;  
 XX  
 DT 20-SEP-1999 (first entry)  
 XX  
 DE Human B-cell myelin oligodendrocyte glycoprotein BMOG.  
 XX  
 KW BMOG; B-cell myelin oligodendrocyte glycoprotein; human;  
 KW signal transduction; immunomodulator; antiinflammatory;  
 KW autoimmune disease; inflammation; gene therapy; diagnosis.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..12  
 FT Protein /note= "leader peptide"  
 FT Modified-site 42  
 FT Modified-site /note= "mature protein"  
 FT Modified-site 68  
 FT Modified-site /note= "N-glycosylated"  
 FT Modified-site 121  
 FT Modified-site /note= "N-glycosylated"  
 FT Domain 139..162  
 FT Peptide /note= "transmembrane domain"  
 FT Peptide 166..177  
 FT /note= "alternatively spliced C-terminal end"  
 XX  
 PN WO9923867-A2.  
 XX  
 PD 20-MAY-1999.  
 XX  
 PF 05-NOV-1998; 98WO-US023826.  
 XX  
 PR 07-NOV-1997; 97US-0064761P.  
 XX  
 PA (BIOJ ) BIOGEN INC.  
 XX  
 PI Browning J;  
 XX  
 DR WPI; 1999-418423/35.  
 DR N-PSDB; AAX59348.  
 XX  
 PT Novel B-cell myelin oligodendrocyte glycoproteins.  
 XX  
 PS Claim 2; Page 43; 43pp; English.  
 XX  
 CC This sequence represents human BMOG, a novel member of the B cell myelin  
 CC oligodendrocyte glycoprotein family that is expressed by germinal centre  
 CC B cells. 3 C-terminal splice variants (see AAY06401-03) of BMOG were  
 CC identified. The protein is present primarily in the spleen, in lymph  
 CC nodes and in germinal centre B cells. It may have immunoregulatory  
 CC functions, and soluble or chimeric fusion proteins of BMOG may be used to  
 CC regulate the immune system in autoimmune or inflammatory disease. Vectors  
 CC comprising BMOG using these transformed host cells are also provided. BMOG  
 CC polypeptides can be used for modulating the immune system of a subject or  
 CC to inhibit signal transduction in a cell expressing BMOG by contacting it  
 CC with a soluble BMOG protein. The nucleic acid can be used for gene  
 CC therapy. The protein can also be used to target a toxin, imaging agent or  
 CC radionuclide to a cell expressing BMOG. (All claimed)  
 XX  
 SQ Sequence 177 AA;  
 Query Match 89.4%; Score 76; DB 2; Length 177;

Best Local Similarity 100.0%; Pred. No. 0.00038;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 WVSQPPPIRTLEGS 14  
 Db 20 WVSQPPPIRTLEGS 33  
 RESULT 7  
 AAY06401  
 ID AAY06401 standard; protein; 190 AA.  
 AC AAY06401;  
 XX  
 DT 20-SEP-1999 (first entry)  
 XX  
 DE Human B-cell myelin oligodendrocyte glycoprotein BMOG.  
 XX  
 KW BMOG; B-cell myelin oligodendrocyte glycoprotein; human;  
 KW signal transduction; immunomodulator; antiinflammatory;  
 KW autoimmune disease; inflammation; gene therapy; diagnosis.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..12  
 FT Protein /note= "leader peptide"  
 FT Modified-site 42  
 FT Modified-site /note= "mature protein"  
 FT Modified-site 68  
 FT Modified-site /note= "N-glycosylated"  
 FT Modified-site 121  
 FT Modified-site /note= "N-glycosylated"  
 FT Domain 139..162  
 FT Peptide /note= "transmembrane domain"  
 FT Peptide 166..190  
 FT /note= "alternatively spliced C-terminal end"  
 XX  
 PN WO9923867-A2.  
 XX  
 PD 20-MAY-1999.  
 XX  
 PF 05-NOV-1998; 98WO-US023826.  
 XX  
 PR 07-NOV-1997; 97US-0064761P.  
 XX  
 PA (BIOJ ) BIOGEN INC.  
 XX  
 PI Browning J;  
 XX  
 DR WPI; 1999-418423/35.  
 DR N-PSDB; AAX59347.  
 XX  
 PT Novel B-cell myelin oligodendrocyte glycoproteins.  
 XX  
 PS Claim 2; Page 42; 43pp; English.  
 XX  
 CC This sequence represents human BMOG, a novel member of the B cell myelin  
 CC oligodendrocyte glycoprotein family that is expressed by germinal centre  
 CC B cells. 3 C-terminal splice variants (see AAY06401-03) of BMOG were  
 CC identified. The protein is present primarily in the spleen, in lymph  
 CC nodes and in germinal centre B cells. It may have immunoregulatory  
 CC functions, and soluble or chimeric fusion proteins of BMOG may be used to  
 CC regulate the immune system in autoimmune or inflammatory disease. Vectors  
 CC comprising BMOG using these transformed host cells are also provided. BMOG  
 CC polypeptides can be used for modulating the immune system of a subject or  
 CC to inhibit signal transduction in a cell expressing BMOG by contacting it  
 CC with a soluble BMOG protein. The nucleic acid can be used for gene  
 CC therapy. The protein can also be used to target a toxin, imaging agent or  
 CC radionuclide to a cell expressing BMOG. (All claimed)

```

XX SQ Sequence 190 AA;
Query Match 89.4%; Score 76; DB 2; Length 190;
Best Local Similarity 100.0%; Pred. No. 0.00041;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVSQPPPIRTLEGS 14
   |||||
Db 20 WVSQPPPIRTLEGS 33

RESULT 8
AAE02769
ID AAE02769 standard; protein; 190 AA.
AC AAE02769;
XX
XX 06-AUG-2001 (first entry)
XX
XX Human NKp30 receptor.
DE
XX Human; NKp30 receptor; natural killer cell; cytostatic; antimicrobial;
KW melanoma; hepatocarcinoma; lung adenocarcinoma; viral infection; tumour;
KW immunosuppressant; antiviral; drug; grafting enhancement; leukaemia;
KW therapy.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..18
XX /label= Signal_peptide
XX Protein 19..190
XX /label= Mature_NKp30_receptor_protein
XX Region 19..138
XX /label= Extracellular_region
XX /note= "Forms an immunoglobulin (Ig) V-like domain"
XX Modified-site 42
XX /note= "N-glycosylation site"
XX FT Modified-site 121
XX /note= "N-glycosylation site"
XX FT Region 139..157
XX /label= Transmembrane_region
XX FT Region 158..190
XX /label= Intracellular_region
XX
XX WO200136630-A2.
XX
XX 25-MAY-2001.
XX
XX 15-NOV-2000; 2000WO-EP011697.
XX
XX 15-NOV-1999; 99CA-02288307.
XX 15-NOV-1999; 99US-00440514.
XX
XX (INNA-) INNATE PHARMA SAS.
XX (UYGE-) UNIV GENOVA.
XX
XX Moretta A, Bottino C, Biassoni R;
XX
XX WPI; 2001-329221/34.
XX N-PSDB; AAD06564.
XX
XX Novel compound, useful for detection and/or quantifying the presence of
XX NK cells, comprises the amino acid sequences of the NKp30 molecule.
XX
XX Claim 1; Fig 7B; 83pp; English.
XX
XX The invention relates to human NKp30 receptor and its corresponding cDNA
XX molecule which is involved in natural cytotoxicity mediated by natural
XX killer (NK) cells and antibodies that identify the same. NKp30 receptor
XX is a member of immunoglobulin super family (Ig-SF). NKp30 is selectively
XX expressed on the surface of human mature NK cells. NKp30 and its cDNA are

```

```

CC useful for detecting and/or quantifying the presence of NK cells in a
CC biological sample. The invention also provide kits for detecting and/or
CC quantifying the presence of NK cells, for the selective removal of NK
CC cells from a biological sample, for the positive and selective
CC purification of NK cells from a biological sample and for the in vitro
CC stimulation of NK cell cytotoxicity. The invention further provides a
CC pharmaceutical composition which is used as a drug for grafting
CC enhancement, graft versus host (GvH) inhibition, stimulation of graft
CC versus tumour (GvT) and especially graft versus leukaemia (GvL), and for
CC the prevention, palliation and/or therapy of solid or liquid tumours,
CC such as melanoma, hepatocarcinoma and lung adenocarcinoma, and/or
CC microorganism, notably viral infection. NKp30 antibodies are useful for
CC identifying NKp30 natural ligands and allow assessment of the level of
CC surface NKp30 ligand expressed on an NK-susceptible target cell and the
CC comparison of this level to the standard physiological one. Hence NKp30
CC antibodies are useful in the diagnosis of tumours or of infection. The
CC present sequence is human NKp30 receptor
XX
XX SQ Sequence 190 AA;

```

```

Query Match 89.4%; Score 76; DB 4; Length 190;
Best Local Similarity 100.0%; Pred. No. 0.00041;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 WVSQPPPIRTLEGS 14
   |||||
Db 20 WVSQPPPIRTLEGS 33

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RESULT 9
AD019810
ID AD019810 standard; protein; 190 AA.
XX
XX AD019810;
XX
XX 12-AUG-2004 (first entry)
XX
XX Human PRO polypeptide #367.
XX
XX Human; PRO; immune related disorder; systemic lupus erythematosus;
XX rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;
XX systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;
XX autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;
XX diabetes mellitus; renal disease; demyelinating disease;
XX central nervous system; peripheral nervous system;
XX demyelinating polyneuropathy; Guillain-Barre syndrome;
XX chronic inflammatory demyelinating polyneuropathy.
XX
XX Homo sapiens.
XX
XX WO2004043361-A2.
XX
XX 27-MAY-2004.
XX
XX 06-NOV-2003; 2003WO-US035268.
XX
XX 08-NOV-2002; 2002US-0425235P.
XX
XX (GETH ) GENENTECH INC.
XX
XX Fong S, Dennis X, Clark H, Chiu H, Schoenfeld J, Williams PM;
XX Wood WI, Wu TD;
XX
XX WPI; 2004-420067/39.
XX N-PSDB; AD019809.
XX
XX Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for
XX treating an immune related disorder such as systemic lupus erythematosus,
XX rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
XX spondyloarthritis.
XX
XX Claim 7; SEQ ID NO 734; 1731pp; English.
XX
XX

```

CC The invention relates to human PRO polypeptides and the polynucleotides  
 CC encoding them. The polypeptides and polynucleotides are useful for  
 CC treating and diagnosing immune related disorders in mammals. The immune  
 CC related disorders include systemic lupus erythematosus, rheumatoid  
 CC arthritis, osteoarthritis, juvenile chronic arthritis, systemic  
 CC sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune  
 CC haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes  
 CC mellitus, immune-mediated renal disease, demyelinating diseases of the  
 CC central or peripheral nervous system, demyelinating polyneuropathy,  
 CC Guillain-Barre syndrome and chronic inflammatory demyelinating  
 CC polyneuropathy. This sequence represents a human PRO polypeptide of the  
 CC invention.

XX SQ Sequence 190 AA;  
 Query Match 89.4%; Score 76; DB 8; Length 190;  
 Best Local Similarity 100.0%; Pred. No. 0.00041;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVSQPPERTLEGS 14  
 |||||  
 DB 20 WVSQPPERTLEGS 33

## RESULT 10

ADQ30923  
 ID ADQ30923 standard; protein; 190 AA.

XX AC ADQ30923;

XX DT 23-SEP-2004 (first entry)

XX DE Human NKp30 polypeptide.

XX KW Natural killer cell; NK cell; NKp30; cytostatic; antimicrobial.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Region 19..138

FT /label= Extracellular region

FT /note= "Region specifically described in Claim 3"

FT Region 20..133

FT /label

FT /note= "Immunogenic peptide specifically described in

FT Claim 3"

FT Region 139..157

FT /label= Transmembrane region

FT /note= "Region specifically described in Claim 3"

FT Region 158..190

FT /label= Cytoplasmic tail

FT /note= "Region specifically described in Claim 3"

XX WO2004056392-A1.

XX PD 08-JUL-2004.

XX XX 22-DEC-2003; 2003WO-BP014716.

XX XX 23-DEC-2002; 2002US-0435344P.

XX PR (INNA-) INNATE PHARMA.

XX PA Rcmagne F, Andre P;

XX PI WPI; 2004-507595/48.

XX DR Pharmaceutical compositions that stimulate proliferation of natural

XX PT killer cells useful for therapy of melanoma, chronic myeloid, and

XX PT leukemia, comprise an anti-natural killer cell receptor antibody and

XX PT interleukins.

XX XX Claim 3; SEQ ID NO 1; 35pp; English.

XX CC The present sequence is that of human NKp30, a 190 amino acid polypeptide  
 CC (about 30 kDa on SDS-PAGE) that is selectively expressed by natural  
 CC killer (NK) cells, and particularly by mature NK cells. Claimed  
 CC pharmaceutical compositions that have a stimulating effect on the  
 CC proliferation of NK cells comprise an antibody such as an anti-NKp30  
 CC antibody or anti-NKp46 antibody or its immuno-reactive fragment and a  
 CC cytokine selected from interleukin-2 (IL2), IL12, IL15 and IL21, the  
 CC antibody(ies) and cytokine(s) being administered together or separately  
 CC to a subject. The anti-NKp30 antibody is an isolated antibody or its  
 CC antigen-binding fragment which specifically binds to NKp30 or to a  
 CC fragment ADQ30924-ADQ30927 of NKp30. The pharmaceutical compositions,  
 CC when used for daily subcutaneous injection, comprising from 1 ng to 100  
 CC mg/kg (body weight) of antibody(ies), and lower than 1 million  
 CC units/square meters/day of cytokine(s), are useful for the prevention,  
 CC palliation and therapy of e.g. melanoma, chronic myeloid leukaemia, acute  
 CC myeloid leukaemia, lymphoma, multiple myeloma, hepatocarcinoma, lung  
 CC adenocarcinoma, neuroblastoma and for antimicrobial prevention,  
 CC palliation and therapy (claimed).

XX SQ Sequence 190 AA;

Query Match 89.4%; Score 76; DB 8; Length 190;

Best Local Similarity 100.0%; Pred. No. 0.00041;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVSQPPERTLEGS 14

|||||

DB 20 WVSQPPERTLEGS 33

## RESULT 11

AA06403

ID AA06403 standard; protein; 201 AA.

XX AC AA06403;

XX DT 20-SEP-1999 (first entry)

XX DE Human B-cell myelin oligodendrocyte glycoprotein BMOG.

XX KW BMOG; B-cell myelin oligodendrocyte glycoprotein; human;

XX signal transduction; immunomodulator; antiinflammatory;

XX autoimmune disease; inflammation; gene therapy; diagnosis.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Peptide 1..12

FT /note= "leader peptide"

FT Protein 13..201

FT /note= "mature protein"

FT Modified-site 42

FT /note= "N-glycosylated"

FT Modified-site 68

FT /note= "N-glycosylated"

FT Modified-site 121

FT /note= "N-glycosylated"

FT Domain 139..162

FT /note= "transmembrane domain"

FT Peptide 166..201

FT /note= "alternatively spliced C-terminal end"

XX WO9923867-A2.

XX PD 20-MAY-1999.

XX XX 05-NOV-1998; 98WO-US023826.

XX PR 07-NOV-1997; 97US-0064761P.

XX PA (BIOJ ) BIOGEN INC.



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PI Browning J;
XX
XX WPI; 1999-418423/35.
DR N-PSDB; AAX59349.
XX
XX Novel B-cell myelin oligodendrocyte glycoproteins.
PT
XX
XX Claim 2; Page 43; 43pp; English.
XX
XX This sequence represents human BMOG, a novel member of the B cell myelin
CC oligodendrocyte glycoprotein family that is expressed by germinal centre
CC B cells' 3 C-terminal splice variants (see AAY06401-03) of BMOG were
CC identified. The protein is present primarily in the spleen, in lymph
CC nodes and in germinal centre B cells. It may have immunoregulatory
CC functions, and soluble or chimeric fusion proteins of BMOG may be used to
CC regulate the immune system in autoimmune or inflammatory disease. Vectors
CC comprising BMOG, prokaryotic and eukaryotic host cells, and a method of
CC producing BMOG using these transformed host cells are also provided. BMOG
CC polypeptides can be used for modulating the immune system of a subject or
CC to inhibit signal transduction in a cell expressing BMOG by contacting it
CC with a soluble BMOG protein. The nucleic acid can be used for gene
CC therapy. The protein can also be used to target a toxin, imaging agent or
CC radionuclide to a cell expressing BMOG. (All claimed)
XX
XX Sequence 201 AA;
SQ
Query Match 89.4%; Score 76; DB 2; Length 201;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WVSQPPPIRTLEGS 14
Db 20 WVSQPPPIRTLEGS 33
RESULT 12
AAE19110
ID AAE19110 standard; protein; 369 AA.
XX
XX AAE19110;
AC
XX
XX 29-AUG-2003 (revised)
DT
XX 21-MAY-2002 (first entry)
DT
XX Human Nkp30-IgG fusion protein.
DE
XX Human; natural killer cell activating protein; Nkp46; therapy; virucide;
KW viral infection; natural killer cell; NK; Nkp44; imaging agent; cancer;
KW detection; carcinoma; melanoma; lymphoma; sarcoma; cytostatic; IgG;
KW immunoglobulin G; fusion protein.
XX
XX Homo sapiens.
OS
XX Chimeric.
OS
XX
XX Key Location/Qualifiers
FH Region 1..135
FT /note= "Human Nkp30"
FT Region 136..369
FT /note= "Human IgG"
XX
XX WO200208287-A2.
XX
XX 31-JAN-2002.
XX
XX 19-JUL-2001; 2001WO-IL000664.
XX
XX 20-JUL-2000; 2000IL-00137419.
XX
XX (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
XX (UYNE ) UNIV BEN-GURION NEGEV.
XX
XX Mandelboim O, Porgador A;
XX

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DR WPI; 2002-195870/25.
DR N-PSDB; AAD30467.
XX
XX New targeting complex capable of targeting an active substance to a
PT target cell, comprising a target recognition segment and an active
PT segment, useful for treating pathologies associated with viral infections
PT or cancer.
XX
XX Example 1; Page 108-110; 113pp; English.
XX
XX The invention relates to compositions and methods for the treatment and
CC detection of a variety of viral infections, by using complex agents
CC comprising the natural killer (NK) cells activating proteins, Nkp46 and
CC Nkp44 and functional fragments thereof, linked to therapeutic or imaging
CC agents. The complex is useful for treating pathologies associated with
CC viral infections (e.g. infections caused by influenza virus, HIV, Epstein
CC -Barr virus, cytomegalovirus, vaccinia virus, ECMV, MVM or herpes virus)
CC and cancer (e.g. carcinomas, melanomas, lymphomas and sarcomas), and for
CC the imaging and monitoring of cancer. The complex may also be used to
CC detect the presence of abnormal cells in a sample. The antibodies can be
CC used to qualitatively or quantitatively detect the ligand for the
CC complex. The present sequence is human Nkp30- immunoglobulin G (IgG) Fc
CC region fusion protein. (Updated on 29-AUG-2003 to standardise OS field)
XX
XX Sequence 369 AA;
SQ
Query Match 89.4%; Score 76; DB 5; Length 369;
Best Local Similarity 100.0%; Pred. No. 0.00082;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WVSQPPPIRTLEGS 14
Db 20 WVSQPPPIRTLEGS 33
RESULT 13
ADP48750
ID ADP48750 standard; protein; 382 AA.
XX
XX ADP48750;
AC
XX
XX 09-SEP-2004 (first entry)
DT
XX Human Nkp30-Fc conjugate protein SEQ ID NO:12.
DE
XX polypeptide conjugate; target recognition; natural killer cell receptor;
KW cytostatic; gene therapy; neoplastic disease; tumour; carcinoma;
KW squamous cell carcinoma; adenocarcinoma; small cell carcinoma; melanoma;
KW glioma; neuroblastoma; B cell lymphoma; T cell lymphoma; leukaemia;
KW human; natural killer cytotoxicity receptor conjugate;
KW Nkp30-Fc conjugate.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Peptide 1..25
FT /label= signal
FT Protein 26..382
FT /note= "Nkp30-Fc conjugate"
FT Misc-difference 26..31
FT /note= "KpnI site"
FT Region 32..148
FT /label= Nkp30
FT Region 149..382
FT /label= Fc
XX
XX WO2004053054-A2.
XX
XX 24-JUN-2004.
XX
XX 09-DEC-2003; 2003WO-IL001040.
XX
XX 09-DEC-2002; 2002US-0431728P.
XX

```

XX PA (NATS-) NATSPEARS LTD.  
 XX PI Mandelboim O, Forgador A;  
 XX DR WPI; 2004-468830/44.  
 XX DR N-PSDB; ADP48757.  
 XX PT New polypeptide conjugate comprising a target recognition segment  
 XX PT comprising a Natural Killer cell receptor consisting of Nkp30, useful in  
 XX PT preparing a composition for treating a neoplastic disease.  
 XX PS Claim 5; SEQ ID NO 4; 66pp; English.  
 XX CC The present invention describes a polypeptide conjugate comprising: (a) a  
 CC target recognition segment comprising a natural killer cell receptor  
 CC (NCR) or its fragment consisting of Nkp30 or its fragment that binds to a  
 CC cellular ligand expressed on the surface of a target tumour cell; and (b)  
 CC a second segment comprising an active agent capable of exerting a  
 CC cytotoxic effect on the target cell. Also described: (1) an isolated  
 CC polynucleotide encoding the polypeptide conjugate; (2) a vector  
 CC comprising the polynucleotide; (3) a host cell comprising the vector and  
 CC capable of expressing the polypeptide conjugate; (4) a pharmaceutical  
 CC composition comprising the polypeptide conjugate and a carrier,  
 CC stabiliser or diluent; (5) treating a neoplastic disease in a subject;  
 CC (6) inhibiting the growth of a tumour in a subject; and (7) delivering a  
 CC cytotoxic substance to a target tumour cell in a subject. The polypeptide  
 CC conjugate has cytostatic activity, and can be used in gene therapy. The  
 CC polypeptide conjugate is useful in preparing a composition for treating a  
 CC neoplastic disease associated with a solid tumour or a non-solid tumour,  
 CC e.g., carcinoma, squamous cell carcinomas, adenocarcinomas, small cell  
 CC carcinomas, melanomas, gliomas, neuroblastomas, B cell lymphoma, T cell  
 CC lymphoma or leukaemia. The present sequence represents a human natural  
 CC killer cytotoxicity receptor conjugate, designated Nkp30-Fc conjugate,  
 CC which is used in the exemplification of the present invention.  
 XX SQ Sequence 382 AA;

Query Match 77.6%; Score 66; DB 6; Length 382;  
 Best Local Similarity 92.9%; Pred. No. 0.036; 1; Indels 0; Gaps 0;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WVSQPPEIRTELEGS 14  
 ||||| |||||  
 Db 33 WVSQPLEIRTELEGS 46

RESULT 14  
 ABB70840  
 ID ABB70840 standard; protein; 1289 AA.  
 XX AC ABB70840;  
 XX DT 26-MAR-2002 (first entry)  
 XX DE Drosophila melanogaster polypeptide SEQ ID NO 39312.  
 XX KW Drosophila; developmental biology; cell signalling; insecticide;  
 XX KW pharmaceutical.  
 XX OS Drosophila melanogaster.  
 XX FN WO200171042-A2.  
 XX PD 27-SEP-2001.  
 XX PF 23-MAR-2001; 2001WO-US009231.  
 XX PR 23-MAR-2000; 2000US-0191637P.  
 XX PR 11-JUL-2000; 2000US-00614150.  
 XX PA (PEXE ) PE CORP NY.  
 XX CC

PI Venter JC, Adams M, Li FWD, Myers EW;  
 XX WPI; 2001-656860/75.  
 DR N-PSDB; ABL14943.  
 XX PT New isolated nucleic acid detection reagent for detecting 1000 or more  
 XX PT genes from Drosophila and for elucidating cell signalling and cell-cell  
 XX PT interactions.  
 XX PS Disclosure; SEQ ID NO 39312; 21pp + Sequence Listing; English.  
 XX CC The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABBS57737,  
 CC ABB72072). The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 1289 AA;

Query Match 57.6%; Score 49; DB 4; Length 1289;  
 Best Local Similarity 81.8%; Pred. No. 72;  
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 QPPRIITLDEGS 14  
 ||||| |||||  
 Db 668 QPPRIITLDEGS 678

RESULT 15  
 ABO58908  
 ID ABO58908 standard; protein; 83 AA.  
 XX AC ABO58908;  
 XX DT 29-JUL-2004 (first entry)  
 XX DE Human genome derived single exon protein #5142.  
 XX KW Human; gene expression; single exon probe; microarray;  
 XX KW alternative splicing event; genomic alteration.  
 XX OS Homo sapiens.  
 XX FN US2003194704-A1.  
 XX PD 16-OCT-2003.  
 XX PF 03-APR-2002; 2002US-00029386.  
 XX PR 03-APR-2002; 2002US-00029386.  
 XX PA (PENN/) PENN S G.  
 XX PA (RANK/) RANK D R.  
 XX PA (HANZ/) HANZEL D K.  
 XX PI Penn SG, Rank DR, Hanzel DK;  
 XX DR WPI; 2004-119264/12.  
 XX CC New human genome-derived single exon nucleic acid probes useful for human  
 XX CC gene expression analysis, for identifying or characterizing alternative  
 XX CC splicing events, for assessing genomic alterations or as tools for  
 XX CC surveying tissues.  
 XX PS Claim 45; SEQ ID NO 32542; 80pp; English.  
 XX CC The invention relates to a nucleic acid probe for measuring human gene  
 XX CC expression, comprising any of the 27,400 fully defined nucleotide

CC sequences in the specification, or their complements or fragments, and  
 CC encoding at least 8 amino acids of any of the 688 amino acid sequences  
 CC fully defined in the specification. The probe is a single exon probe that  
 CC hybridises under high stringency conditions to a nucleic acid molecule  
 CC expressed in human cells or tissues. Also included are a spatially-  
 CC addressable set of single exon nucleic acid probes for measuring human  
 CC gene expression (comprising a plurality of single exon nucleic acid  
 CC probes cited above, where each of the plurality of probes is separately  
 CC and addressably isolatable or amplifiable from the plurality), a single  
 CC exon microarray for measuring human gene expression, a method of  
 CC measuring human gene expression, a vector comprising the single exon  
 CC probe cited above, an ORF-encoded peptide comprising at least 8  
 CC contiguous amino acids of any of the above-mentioned amino acid  
 CC sequences (optionally with conservative amino acid substitutions), an  
 CC isolated antibody that binds specifically to a peptide cited above,  
 CC methods of selling and/or licensing single exon probes or microarrays to  
 CC a customer desiring to measure gene expression, a method of providing  
 CC human gene expression data by subscription, and a computer-readable  
 CC storage medium which contains a database having a plurality of records  
 CC (each record including data on the expression of a single exon probe  
 CC cited above. The probe, methods and apparatus are useful in gene  
 CC expression analysis. The probes may be used as tools for surveying  
 CC tissues to detect the presence of expressed messages that contain their  
 CC specific exon, or in constructing genome-derived single exon microarrays.  
 CC In addition, the probes are used in identifying and characterising  
 CC alternative splicing events, in detecting and characterising gross  
 CC alterations in the genomic locus that includes their exon, in assessing  
 CC smaller genomic alterations, in priming the synthesis of nucleic acids,  
 CC or in expressing the ORF-encoded peptide. The present sequence is a human  
 CC single exon probe protein of the invention. Note: The sequence data for  
 CC this patent did not form part of the printed specification, but was  
 CC obtained in electronic format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html?DocID=20030194704

XX  
 SQ Sequence 83 AA;

Query Match 53.5%; Score 45.5; DB 8; Length 83;

Best Local Similarity 50.0%; Pred. No. 16;

Matches 9; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 1 WVSQPPPIRTLEGSC 15

Db 24 W-SRPPELRPWGSC 37

Search completed: November 16, 2004, 18:56:04  
 Job time : 18.9549 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 16, 2004, 19:14:52 ; Search time 13.4085 Seconds  
(without alignments)  
395.815 Million cell updates/sec

Title: US-10-036-444-7

Perfect score: 85

Sequence: 1 WVSQPEIRTEGSC 15

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1568699 segs, 353819137 residues

Total number of hits satisfying chosen parameters: 1568699

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:  
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5: /cgn2\_6/ptodata/1/pubaa/US07\_NEW\_PUB.pep.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	100.0	15	13	US-10-036-444-7
2	76	89.4	120	13	US-10-036-444-7
3	76	89.4	135	15	US-10-333-481-17
4	76	89.4	161	16	US-10-696-259-10
5	76	89.4	177	16	US-10-696-259-5
6	76	89.4	190	13	US-10-036-444-2
7	76	89.4	190	16	US-10-696-259-4
8	76	89.4	201	16	US-10-696-259-6
9	76	89.4	369	15	US-10-333-481-18
10	61.5	72.4	175	16	US-10-696-259-8
11	61.5	72.4	185	16	US-10-696-259-7
12	61.5	72.4	198	16	US-10-696-259-9
13	50	58.8	71	15	US-10-424-593-173742

14	48	56.5	275	15	US-10-424-599-146488	Sequence 146488,
15	48	56.5	1517	14	US-10-156-761-14713	Sequence 14713, A
16	46	54.1	343	16	US-10-437-963-148764	Sequence 148764,
17	46	54.1	429	16	US-10-437-963-190212	Sequence 190212,
18	45.5	53.5	83	14	US-10-029-386-32542	Sequence 32542, A
19	43	50.6	80	16	US-10-437-963-168450	Sequence 168450,
20	43	50.6	108	15	US-10-424-599-195126	Sequence 195126,
21	43	50.6	154	15	US-10-424-599-192301	Sequence 192301,
22	43	50.6	514	15	US-10-014-099F-59	Sequence 59, Appl
23	42	49.4	236	17	US-10-425-115-193065	Sequence 193065,
24	42	49.4	273	17	US-10-425-115-236668	Sequence 236668,
25	42	49.4	341	17	US-10-425-115-193062	Sequence 193062,
26	42	49.4	360	15	US-10-425-115-64090	Sequence 64090, A
27	42	49.4	383	15	US-10-282-122A-67247	Sequence 67247, A
28	42	49.4	451	9	US-09-902-772-2	Sequence 2, Appl
29	42	49.4	462	13	US-10-087-192-1128	Sequence 1128, Ap
30	42	49.4	462	14	US-10-085-823-99	Sequence 99, Appl
31	42	49.4	462	14	US-10-021-660-95	Sequence 95, Appl
32	42	49.4	462	15	US-10-211-462-42	Sequence 42, Appl
33	42	49.4	478	9	US-09-902-772-4	Sequence 4, Appl
34	42	49.4	1317	9	US-09-815-242-5118	Sequence 5118, Ap
35	42	49.4	1317	15	US-10-282-122A-43495	Sequence 43495, A
36	41.5	48.8	116	15	US-10-364-049-3423	Sequence 3423, Ap
37	41	48.2	59	15	US-10-424-599-158229	Sequence 158229,
38	41	48.2	78	16	US-10-767-701-60904	Sequence 60904, A
39	41	48.2	87	11	US-09-864-408A-5014	Sequence 5014, Ap
40	41	48.2	96	17	US-10-425-115-220003	Sequence 220003,
41	41	48.2	137	10	US-09-947-063-2	Sequence 2, Appl
42	41	48.2	137	10	US-09-947-063-5	Sequence 5, Appl
43	41	48.2	146	17	US-10-425-115-229735	Sequence 229735,
44	41	48.2	175	17	US-10-425-115-341865	Sequence 341865,
45	41	48.2	339	14	US-10-369-493-16318	Sequence 16318, A

#### ALIGNMENTS

##### RESULT 1

US-10-036-444-7  
; Sequence, Application US/10036444  
; Publication No. US20020142445A1  
; GENERAL INFORMATION:  
; APPLICANT: INNATE PHARMA S.A.S.  
; APPLICANT: UNIVERSITA DI GENOVA  
; TITLE OF INVENTION: "No. US20020142445A1e1 triggering receptor involved in natural  
; TITLE OF INVENTION: cytotoxicity mediated by human Natural Killer cells and  
; TITLE OF INVENTION: antibodies that identify the same"  
; FILE REFERENCE: SEQ-FR-1060  
; CURRENT APPLICATION NUMBER: US/10/036.444  
; CURRENT FILING DATE: 2002-01-07  
; PRIOR APPLICATION NUMBER: 09/440,514  
; PRIOR FILING DATE: 1999-11-15  
; PRIOR APPLICATION NUMBER: 09/456,199  
; PRIOR FILING DATE: 1999-12-07  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence

FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:peptide derived  
; OTHER INFORMATION: from natural sequence, useful for antiserum  
; OTHER INFORMATION: production  
US-10-036-444-7

Query Match 100.0%; Score 85; DB 13; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVSQPEIRTEGSC 15

DB 1 WVSQPEIRTEGSC 15

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RESULT 2
US-10-036-444-4
; Sequence 4, Application US/10036444
; Publication No. US20020142445A1
; GENERAL INFORMATION:
; APPLICANT: INNATE PHARMA S.A.S.
; TITLE OF INVENTION: "No. US20020142445A1 triggering receptor involved in natural
; TITLE OF INVENTION: cytotoxicity mediated by human Natural Killer cells and
; TITLE OF INVENTION: antibodies that identify the same"
; FILE REFERENCE: SEQ-FR-1080
; CURRENT APPLICATION NUMBER: US/10/036,444
; CURRENT FILING DATE: 2002-01-07
; PRIOR FILING DATE: 1999-11-15
; PRIOR APPLICATION NUMBER: 09/440,514
; PRIOR FILING DATE: 1999-11-15
; PRIOR APPLICATION NUMBER: 09/456,199
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Human NK cell
US-10-036-444-4

Query Match      89.4%; Score 76; DB 13; Length 120;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVSQPPEIRTEG 14
Db 2 WVSQPPEIRTEG 15

RESULT 3
US-10-333-481-17
; Sequence 17, Application US/10333481
; Publication No. US20040072256A1
; GENERAL INFORMATION:
; APPLICANT: Ofer Mandelboim
; APPLICANT: Angel Porcador
; TITLE OF INVENTION: NK CELLS ACTIVATING RECEPTORS AND THEIR THERAPEUTIC AND DIAGNOSTIC
; FILE REFERENCE: 68657
; CURRENT APPLICATION NUMBER: US/10/333,481
; CURRENT FILING DATE: 2003-08-04
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: PCT/IL01/00664
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 135
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-333-481-17

Query Match      89.4%; Score 76; DB 15; Length 135;
Best Local Similarity 100.0%; Pred. No. 0.00049;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVSQPPEIRTEG 14
Db 20 WVSQPPEIRTEG 33

RESULT 4
US-10-696-259-10
; Sequence 10, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-10

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Best Local Similarity 100.0%; Pred. No. 0.00064;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVSQPPEIRTEG 14
Db 20 WVSQPPEIRTEG 33

RESULT 5
US-10-696-259-5
; Sequence 5, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-5

Query Match      89.4%; Score 76; DB 16; Length 161;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVSQPPEIRTEG 14
Db 20 WVSQPPEIRTEG 33

RESULT 6
US-10-036-444-2
; Sequence 2, Application US/10036444
; Publication No. US20020142445A1
; GENERAL INFORMATION:
; APPLICANT: INNATE PHARMA S.A.S.
; APPLICANT: UNIVERSITA DI GENOVA
; TITLE OF INVENTION: "No. US20020142445A1 triggering receptor involved in natural
```

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; TITLE OF INVENTION: cytotoxicity mediated by human Natural Killer cells and
; TITLE OF INVENTION: antibodies that identify the same"
; FILE REFERENCE: SEQ-PR-1060
; CURRENT APPLICATION NUMBER: US/10/036,444
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 09/440,514
; PRIOR FILING DATE: 1999-11-15
; PRIOR APPLICATION NUMBER: 09/456,199
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Human NK cell
US-10-036-444-2

Query Match      89.4%; Score 76; DB 13; Length 190;
Best Local Similarity 100.0%; Pred. No. 0.00069;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WVSQPPEIRLTLEGS 14
      |||||
Db      20 WVSQPPEIRLTLEGS 33

RESULT 7
US-10-696-259-4
; Sequence 4, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-4

Query Match      89.4%; Score 76; DB 16; Length 190;
Best Local Similarity 100.0%; Pred. No. 0.00069;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WVSQPPEIRLTLEGS 14
      |||||
Db      20 WVSQPPEIRLTLEGS 33

RESULT 8
US-10-696-259-6
; Sequence 6, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
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; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-6

Query Match      89.4%; Score 76; DB 16; Length 201;
Best Local Similarity 100.0%; Pred. No. 0.00073;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WVSQPPEIRLTLEGS 14
      |||||
Db      20 WVSQPPEIRLTLEGS 33

RESULT 9
US-10-333-481-18
; Sequence 18, Application US/10333481
; Publication No. US20040072256A1
; GENERAL INFORMATION:
; APPLICANT: Ofet Mandelboim
; APPLICANT: Angel Porgador
; TITLE OF INVENTION: NK CELLS ACTIVATING RECEPTORS AND THEIR THERAPEUTIC AND DIAGNOSI
; FILE REFERENCE: 68657
; CURRENT APPLICATION NUMBER: US/10/333,481
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: PCT/IL01/00664
; PRIOR FILING DATE: 2001-07-19
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 18
; LENGTH: 369
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-333-481-18

Query Match      89.4%; Score 76; DB 15; Length 369;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WVSQPPEIRLTLEGS 14
      |||||
Db      20 WVSQPPEIRLTLEGS 33

RESULT 10
US-10-696-259-8
; Sequence 8, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; FILE REFERENCE: A041 US
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; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-8

Query Match      72.4%; Score 61.5; DB 16; Length 175;
Best Local Similarity 92.9%; Pred. No. 0.12;
Matches 13; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 WVSQPEIRTEG 14
Db 20 WVSQPEIRTEG 32

RESULT 11
US-10-696-259-7
; Sequence 7, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-7

Query Match      72.4%; Score 61.5; DB 16; Length 185;
Best Local Similarity 92.9%; Pred. No. 0.13;
Matches 13; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 WVSQPEIRTEG 14
Db 20 WVSQPEIRTEG 32

RESULT 12
US-10-696-259-9
; Sequence 9, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07

; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-9

Query Match      72.4%; Score 61.5; DB 16; Length 198;
Best Local Similarity 92.9%; Pred. No. 0.14;
Matches 13; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 WVSQPEIRTEG 14
Db 20 WVSQPEIRTEG 32

RESULT 13
US-10-424-599-173742
; Sequence 173742, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 173742
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_127908C.1.pap
US-10-424-599-173742

Query Match      58.8%; Score 50; DB 15; Length 71;
Best Local Similarity 64.3%; Pred. No. 3.3;
Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 WVSQPEIRTEG 14
Db 8 WTPSPPHIRTEG 21

RESULT 14
US-10-424-599-146488
; Sequence 146488, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 146488
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(275)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
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Job time : 14.4085 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 16, 2004, 19:04:36 ; Search time 4.21751 Seconds  
(without alignments)  
235.867 Million cell updates/sec

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Perfect score: 85  
Sequence: , 1 WVSQPPEIRTEGSC 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Issued Patents AA:**
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3: /cgn2_6/ptodata/1/iaa/6A_COMB.rep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.rep.*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.rep.*
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## SUMMARIES

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1	42	49.4	134	4	US-09-513-999C-5417	Sequence 5417, Ap
2	42	49.4	451	3	US-08-878-177-2	Sequence 2, Appli
3	42	49.4	478	3	US-08-878-177-4	Sequence 4, Appli
4	42	49.4	1128	4	US-09-252-991A-1032	Sequence 31032, A
5	41	48.2	170	4	US-09-270-767-36791	Sequence 36791, A
6	41	48.2	170	4	US-09-270-767-52008	Sequence 52008, A
7	41	48.2	249	3	US-09-189-760-6	Sequence 6, Appli
8	41	48.2	249	3	US-09-189-811-6	Sequence 6, Appli
9	41	48.2	249	3	US-09-514-423-6	Sequence 6, Appli
10	41	48.2	289	4	US-09-673-395A-155	Sequence 155, App
11	41	48.2	314	4	US-09-248-796A-17233	Sequence 17233, A
12	41	48.2	478	4	US-09-134-000C-6219	Sequence 6219, Ap
13	41	48.2	517	3	US-09-189-760-2	Sequence 2, Appli
14	41	48.2	517	3	US-09-514-423-2	Sequence 2, Appli
15	41	48.2	567	3	US-09-188-811-2	Sequence 2, Appli
16	40	47.1	84	4	US-09-135-2388-4	Sequence 4, Appli
17	40	47.1	196	4	US-09-492-709A-376	Sequence 376, App
18	40	47.1	202	4	US-09-328-352-5586	Sequence 5586, Ap
19	40	47.1	344	4	US-09-252-991A-31357	Sequence 31357, A
20	39	45.9	146	4	US-09-252-991A-32438	Sequence 32438, A
21	39	45.9	309	4	US-09-270-767-44392	Sequence 44392, A
22	39	45.9	650	4	US-09-489-039A-7678	Sequence 7678, Ap
23	39	45.9	788	4	US-09-248-796A-20511	Sequence 20511, A
24	38	44.7	353	4	US-09-252-991A-19842	Sequence 19842, A
25	38	44.7	409	1	US-08-190-802A-51	Sequence 51, Appli
26	38	44.7	409	2	US-08-283-917-3	Sequence 3, Appli
27	38	44.7	409	2	US-08-961-716-3	Sequence 3, Appli

Sequence 51, Appl  
Sequence 51, Appl  
Sequence 51, Appl  
Sequence 119, Ap  
Sequence 9, Appl  
Sequence 9, Appl  
Sequence 732, Ap  
Sequence 7732, Ap  
Sequence 7582, Ap  
Sequence 1, Appl  
Sequence 2, Appl  
Sequence 2, Appl  
Sequence 2, Appl  
Sequence 1, Appl  
Sequence 1, Appl  
Sequence 387, App  
Sequence 387, App  
Sequence 387, App  
Sequence 387, App

## ALIGNMENTS

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RESULT 1
US-09-513-999C-5417
; Sequence 5417, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,
; CURRENT FILING DATE: 2000-02-24

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Query Match 49.4%; Score 42; DB 4; Length 134;  
Best Local Similarity 46.7%; Pred. No. 23;  
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 WVSQPPEIRTEGSC 15  
|:|:|:|:|  
Db 56 WLSOPPARVTIMEC 70

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RESULT 2
US-08-878-177-2
; Sequence 2, Application US/08878177
; Patent No. 6294354
; GENERAL INFORMATION:
; APPLICANT: Chugai Seiyaku Kabushiki
; TITLE OF INVENTION: Cell Calcifica
; TITLE OF INVENTION: The Proteins
; FILE REFERENCE: chugai sei'yaku kab
; CURRENT APPLICATION NUMBER: US/08/

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; EARLIER APPLICATION NUMBER: 09/163,116
; EARLIER FILING DATE: 1998-09-29
; EARLIER APPLICATION NUMBER: 60/089,467
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: (PENDING)
; EARLIER FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-189-760-6

Query Match      48.2%; Score 41; DB 3; Length 249;
Best Local Similarity 35.7%; Pred. No. 65;
Matches 5; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY      1 WVSQPPEIRTELEGS 14
Db      181 WIETPPSIKSLDSN 194

RESULT 8
US-09-188-811-6
; Sequence 6, Application US/09188811
; Patent No. 6037148
; GENERAL INFORMATION:
; APPLICANT: Khodadoust, Mehran
; TITLE OF INVENTION: NOVEL MTBX PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCES: THEREFOR
; FILE REFERENCES: MNI-046CP
; CURRENT APPLICATION NUMBER: US/09/188,811
; CURRENT FILING DATE: 1998-11-09
; EARLIER APPLICATION NUMBER: 09/163,116
; EARLIER FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-188-811-6

Query Match      48.2%; Score 41; DB 3; Length 249;
Best Local Similarity 35.7%; Pred. No. 65;
Matches 5; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY      1 WVSQPPEIRTELEGS 14
Db      181 WIETPPSIKSLDSN 194

RESULT 9
US-09-514-422-6
; Sequence 6, Application US/095:4422
; Patent No. 6291193
; GENERAL INFORMATION:
; APPLICANT: Khodadoust, Mehran
; TITLE OF INVENTION: NOVEL MTBX PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCES: THEREFOR
; FILE REFERENCES: MNI-046CP2
; CURRENT APPLICATION NUMBER: US/09/514,422
; CURRENT FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: US/09/189,760
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/163,116
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/089,467
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: (PENDING)
; PRIOR FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 10
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-514-422-6

Query Match      48.2%; Score 41; DB 3; Length 249;
Best Local Similarity 35.7%; Pred. No. 65;
Matches 5; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY      1 WVSQPPEIRTELEGS 14
Db      181 WIETPPSIKSLDSN 194

RESULT 10
US-09-673-395A-155
; Sequence 155, Application US/09673395A
; Patent No. 6620923
; GENERAL INFORMATION:
; APPLICANT: SPECHT, THOMAS
; APPLICANT: HINZMANN, BERND
; APPLICANT: SCHMITT, ARMIN
; APPLICANT: PILARSKY, CHRISTIAN
; APPLICANT: DAHL, EDGAR
; APPLICANT: ROSENTHAL, ANDRE
; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM UTERUS TUMOR TISSUE
; FILE REFERENCE: ALBRE-12
; CURRENT APPLICATION NUMBER: US/09/673,395A
; CURRENT FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 637
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 155
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-673-395A-155

Query Match      48.2%; Score 41; DB 4; Length 289;
Best Local Similarity 46.7%; Pred. No. 76;
Matches 7; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY      1 WVSQPPEIRTELEGSC 15
Db      267 WQQPPAARSCYGLC 281

RESULT 11
US-09-248-796A-17233
; Sequence 17233, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 17233
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-17233

Query Match      48.2%; Score 41; DB 4; Length 314;
Best Local Similarity 58.3%; Pred. No. 83;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
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QY      1 WVSQPPPIRTLE 12
Db      302 WVNQPPPIRTKE 313

RESULT 12
US-09-134-000C-6219
; Sequence 6219, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6219
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-6219

Query Match      48.2%; Score 41; DB 4; Length 478;
Best Local Similarity 40.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY      1 WVSQPPPIRTLE 15
Db      290 WIEMPPPIRTLE 304

RESULT 13
US-09-189-760-2
; Sequence 2, Application US/09189760
; Patent No. 6031078
; GENERAL INFORMATION:
; APPLICANT: Khodadoust, Mehran
; TITLE OF INVENTION: NOVEL MTBX PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: MNI-046CP2
; CURRENT APPLICATION NUMBER: US/09/189,760
; CURRENT FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 09/163,116
; EARLIER FILING DATE: 1998-09-29
; EARLIER APPLICATION NUMBER: 60/089,467
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: (PENDING)
; EARLIER FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-189-760-2

Query Match      48.2%; Score 41; DB 3; Length 517;
Best Local Similarity 35.7%; Pred. No. 1.4e+02;
Matches 5; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY      1 WVSQPPPIRTLE 14
Db      449 WIETPPSIKSLDSN 462

RESULT 14
US-09-514-422-2
; Sequence 2, Application US/09514422
; Patent No. 6291193
; GENERAL INFORMATION:
; APPLICANT: Khodadoust, Mehran
; TITLE OF INVENTION: NOVEL MTBX PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: MNI-046CP2
; CURRENT APPLICATION NUMBER: US/09/514,422
; CURRENT FILING DATE: 2000-02-28
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/163,116
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/089,467
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: (PENDING)
; PRIOR FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-514-422-2

Query Match      48.2%; Score 41; DB 3; Length 517;
Best Local Similarity 35.7%; Pred. No. 1.4e+02;
Matches 5; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY      1 WVSQPPPIRTLE 14
Db      449 WIETPPSIKSLDSN 512

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3	116	11.4	146	2	B26408
4	107.5	10.5	138	2	C27577
5	106.5	10.4	131	2	E24092
6	106.5	10.4	131	2	E24092
7	106	10.4	132	1	RWMSAV
8	105	10.3	131	2	F45893
9	104.5	10.2	132	2	S03713
10	103	10.1	129	2	A42692
11	102.5	10.0	110	2	B24092
12	101.5	10.0	139	2	S36325
13	101	9.9	120	2	I54487
14	100	9.8	130	2	A24092
15	99	9.7	130	2	A31211
16	98.5	9.7	128	2	S24319
17	98.5	9.7	152	2	S21826
18	96	9.4	131	1	L6FUEB
19	96	9.4	131	2	D24402
20	95.5	9.4	140	2	PH0134
21	94.5	9.3	108	2	JH0342
22	94.5	9.3	186	2	S08614
23	93	9.1	117	2	I68824
24	93	9.1	132	2	A45893
25	92.5	9.1	136	2	S42610
26	92.5	9.1	139	2	S6302
27	92	9.0	129	2	A30554
28	91.5	8.9	107	2	S60590
29	90.5	8.9	145	2	S21651

Over, Match

Query Match 11.5%; Score 117.5; DB 2; Length 132;

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Best Local Similarity 30.8%; Pred. No. 0.0018;
Matches 44; Conservative 17; Mismatches 47; Indels 35; Gaps 9;

QY 12 VHGSGCALW-----VSQPP-IRTLGSSAFPCSNASQGRLAIGSVTWFRDE 59
DB 3 LHVSLVFLWLQLGSSQKXVQSPSLVPEGAMVSLNCSFSDS-----ASQSIWYQQH 58
QY 60 VVPGKEVR-----NGTPEFRGLAPLASSRFLHDHQAELHIRDVGRGHDAIYVCRVEV 112
DB 59 --FGKPKALISIFSGNKK-EGRLTVYLNRAHLA---VSLHKQSPSDSAVYLCAVR 112

QY 113 LGLGVGT---GNCTRLVWEKEHP 132
DB 113 SGANTGKLFHGHTILRV---HP 132

RESULT 3
S26408
T-cell receptor beta chain V region (5.5) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S26408
R: Bowman, S.J.; Lanchbury, J.S.
submitted to the EMBL Data Library, September 1992
A:Description: T cell receptor beta chain sequences from patients with rheumatoid arthritis
A:Reference number: S26408
A:Status: preliminary
A:Accession: S26408
A:Molecule type: mRNA
A:Residues: 1-146 <BOW>
A:Cross-references: EMBL:X68527; NID:G36172; PIDN:CAA48540.1; PID:G36173
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor
F:35-112/Domain: immunoglobulin homology <IMM>

Query Match 11.4%; Score 116; DB 2; Length 146;
Best Local Similarity 26.5%; Pred. No. 0.0027;
Matches 39; Conservative 26; Mismatches 52; Indels 30; Gaps 7;

QY 1 MAMVLLILLIMVHGSCALWVSQPP-IRTLGSSAFPCSNASQGRLAIGSVTWFRD 58
DB 6 LCWVLLCLL---GAGSVETGVTQSPHLLIKT-RGQVTLRCSSQSGH-----NTVSWYQQ 56
QY 59 EVVPG-----KEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVGRGHDAIYVCRV 110
DB 57 ALCGGQPFQIYYREBNG-----RGNFPFRGSLQFPNYSSSLNVNVALELDDSDALYLCA 112

QY 111 EVLGLGVGT-----GNCTRLVWEKE 130
DB 113 SPKGLGLPSRGYQYFGPGTRLVTTED 139

RESULT 4
C27577
T-cell receptor alpha chain V region (5/10-20D) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 30-May-1997
C:Accession: C27577; C27557
R: Awamoto, A.; Onashi, P.S.; Bircher, H.; Walker, C.B.; Michalopoulos, E.E.; Rupp, F.; H.
J. Exp. Med. 165, 591-600, 1987
A:Title: T cell receptor variable gene usage in a specific cytotoxic T cell response. PI
A:Reference number: A27557; MUID:87139812; PMID:3493320
A:Accession: C27577
A:Molecule type: mRNA
A:Residues: 1-138 <IWA>
A:Accession: C27557
A:Molecule type: mRNA
A:Residues: 22-138 <IWT>
A:Cross-references: EMBL:X05733
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor

Query Match 10.5%; Score 107.5; DB 2; Length 138;

```

```

Best Local Similarity 31.9%; Pred. No. 0.015;
Matches 38; Conservative 17; Mismatches 45; Indels 19; Gaps 7;

QY 21 VSQPP-IRTLGSSAFPCSNASQGRLAIGSVTWFRDEVPKQVR-----NGTPE 72
DB 24 VQSPESLIVPEGAMVSLNCTFSDASQY----FAMIRQH--SGKAPKALMSIFSNGEKE 77
QY 73 FRRLAPLASSRFLHDHQAELHIRDVGRGHDAIYVCRVEVL-GLGVGTGNGTRLVWEKE 130
DB 78 -EGFTTHLKASLH---PSLHIRDSPSDSALYLCAVSMTGKVKVFGSGTRLVSPD 132

RESULT 5
D24092
T-cell receptor alpha chain precursor V region (B10) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 19-Nov-1988 #sequence_revision 01-Dec-2000 #text_change 11-Jan-2002
C:Accession: D24092; S03507
R: Fink, P.J.; Matis, L.A.; McElligott, D.L.; Bookman, M.; Hedrick, S.M.
Nature 321, 219-226, 1986
A:Title: Correlations between T-cell specificity and the structure of the antigen receptor
A:Reference number: A93380; MUID:86230843; PMID:3012351
A:Accession: D24092
A:Molecule type: mRNA
A:Residues: 1-131 <FIN>
R: Winoto, A.; Mjolsness, S.; Hood, L.
Nature 316, 832-836, 1985
A:Title: Genomic organization of the genes encoding mouse T-cell receptor alpha-chain.
A:Reference number: S03503; MUID:85296332; PMID:2993908
A:Accession: S03507
A:Molecule type: DNA
A:Residues: 111-130 <WIN>
A:Cross-references: EMBL:X03057; NID:G54519; PIDN:CAA26864.1; PID:gl334131
A:Note: This sequence was determined from the germline gene
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-131/Product: T-cell receptor alpha chain V region B10 #status predicted <MAT>
F:36-109/Domain: immunoglobulin homology <IMM>

Query Match 10.4%; Score 106.5; DB 2; Length 131;
Best Local Similarity 29.6%; Pred. No. 0.017;
Matches 37; Conservative 19; Mismatches 42; Indels 27; Gaps 7;

QY 21 VSQPP-IRTLGSSAFPCSNASQGRLAIGSVTWF---RDEVVPGKEVRNGTPEFRG 75
DB 24 VEQSPSALSLEHGSGSALRCNFTT-----MRAVQWFRKNSRGSLLNLFYASGTKE-NG 77
QY 76 RLAPLASSRFLHDHQAELHIRDVGRGHDAIYVCRVEVLGLGVGTGNGTRLVWEKEHPQLG 135
DB 78 RLKSAFDSK---ERYSTLHIDAQLDSDGYTCAAE-----ATSSGQKLV-----FG 131

QY 136 AGTVL 140
DB 122 QGTVL 126

RESULT 6
E24092
T-cell receptor alpha chain precursor V region (4.C3) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 21-Jan-2000
C:Accession: E24092
R: Fink, P.J.; Matis, L.A.; McElligott, D.L.; Bookman, M.; Hedrick, S.M.
Nature 321, 219-226, 1986
A:Title: Correlations between T-cell specificity and the structure of the antigen receptor
A:Reference number: A93380; MUID:86230843; PMID:3012351
A:Accession: E24092
A:Molecule type: mRNA
A:Residues: 1-131 <FIN>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor
F:1-20/Domain: signal sequence #status predicted <SIG>

```



```

RESULT 8
F45893
T-cell receptor alpha chain precursor V region (BT25) - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 20-Jun-2000
C;Accession: F45893
R;Ishiguro, N.; Tanaka, A.; Shinagawa, M.
Immunogenetics 31, 57-60, 1990
A;Title: Sequence analysis of bovine T-cell receptor alpha chain.
A;Reference number: F45893; NUID:90129157; PMID:2137108
A;Accession: F45893
A;Status: Preliminary

```

```

RESULT 10
A42692
T-cell receptor alpha chain (lysozyme peptide specific) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C:Accession: A42692
R:Kobori, J.A.; Hood, L.; Shastri, N.
Proc. Natl. Acad. Sci. U.S.A. 89, 2940-2944, 1992
A:Title: Structure-function relationship among T-cell receptors specific for lysozyme i
A:Reference number: A42692; MUID:92212944; PMID:1313573
A:Accession: A42692
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-129 <KOB>
A:Cross-references: GB:M87844; NID:g201804; PID:AAA51236.1; PID:G554375
A:Experimental source: T-cell hybrid B04H.9.1
A:Note: sequence extracted from NCBI backbone (NCBIN:92850. NCBIIP:92851)

```

C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: T-cell receptor  
F;35-109/Domain: immunoglobulin homology <IMM>

Query Match 10.1%; Score 103; DB 2; Length 129;  
Best Local Similarity 29.8%; Pred. No. 0.035;  
Matches 39; Conservative 14; Mismatches 34; Indels 44; Gaps 8;

QY 20 WVS-----QPPRTLEGSSAFPCSFNASQGLAIGSVTFRD-----VVP 63  
DB 18 WSGDKVKQSPSALSQEGTNSALRCNFS-----IAATVQFLQNGRSLINLYLP- 71  
QY 64 KEVRNGTPEFRGRAPLASSRFLHDHQAELHIRDVRGHDASIVCRVEVLGSGVTGN-- 121  
DB 72 -----GTKE-NGRKSAFDSK---ESYSTLHIRDAQLEDSTGYFCAAE-----DTGNV 116  
QY 122 -----GTRLVY 127  
DB 117 YVEGAGTRLUK 127

## RESULT 11

B24092  
T-cell receptor alpha chain V region (5C.C7) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 21-Jan-2000  
C;Accession: B24092  
R;Pink, P.J.; Matis, L.A.; McElligott, D.L.; Bookman, M.; Hedrick, S.M.  
Nature 321, 219-226, 1986  
A;Title: Correlations between T-cell specificity and the structure of the antigen receptor  
A;Reference number: A93380; MUID:86230843; PMID:3012351  
A;Accession: B24092  
A;Molecule type: mRNA  
A;Residues: 1-110 <FIN>  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: T-cell receptor  
F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 10.0%; Score 102.5; DB 2; Length 110;  
Best Local Similarity 31.9%; Pred. No. 0.033;  
Matches 36; Conservative 16; Mismatches 46; Indels 15; Gaps 6;

QY 21 VSQPPERTL-EGSSAFPCSFNASQGLAIGSVTFRD-----RDEVVPGKEVRNGTPEFRG 75  
DB 4 VEQSPSALSHEGTDSALRCNFTTT-----MRVQVFRKNRSGSLINLYLASGTKE-NG 57  
QY 76 RLAPLASSRFLHDHQAELHIRDVRGHDASIVCRVEVLGLG-VGTGNGTRLVY 127  
DB 58 RLKSAFDSK---ERYSTLHIRDAQLEDSTGYFCAAEASNTNKVFGTGRLOV 107

## RESULT 12

S36325  
T-cell receptor delta chain precursor - sheep (fragment)  
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 21-Jan-2000  
C;Accession: S36325; S23040  
R;Hein, W.R.; Dudler, L.  
EMBO J. 12, 715-724, 1993  
A;Title: Divergent evolution of T cell repertoires: extensive diversity and development  
A;Reference number: S36287; MUID:93178447; PMID:8440261  
A;Accession: S36325  
A;Status: preliminary; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-139 <HEI>  
A;Cross-references: EMBL:Z12997; NID:G2258; PIDN:CAA78341.1; PID:G2259  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: T-cell receptor  
F;33-113/Domain: immunoglobulin homology <IMM>

Query Match 10.0%; Score 101.5; DB 2; Length 139;  
Best Local Similarity 29.7%; Pred. No. 0.052;  
Matches 41; Conservative 14; Mismatches 60; Indels 23; Gaps 7;

QY 9 LIMVHFGSCALWVSQ-PPEIRTLLEGSSAFPCSFNASQGLAIGSVTFRD---DEVVPGK 64  
DB 9 LLLFYKGLVCLNQVTQSSPEQVRASGREVTLCQTFQITYSN---PDLYWYRKTDPAVFQFV 65  
QY 65 EVRNGTPEFRGRAPLASSRFLHDHQA-----ELHIRDVRGHDASIVCRVEVLGLGV-- 117  
DB 66 LYRDNT---RSRDADFARGFTVQHSVRSKTFELVSVSRPEDTATYYCALD-LQRGIYD 121  
QY 118 -----GTGNGTRLVVEKE 130  
DB 122 TTDKLTFFGKTRLIVEPE 139

## RESULT 13

I54487  
T-cell receptor alpha chain - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 09-Jul-2004  
C;Accession: I54487; I68823  
R;Nakajima, P.B.; Di Vincenzo, J.P.; Jameson, S.C.; Gascoigne, N.R.J.  
Immunogenetics 35, 190-198, 1992  
A;Title: Chromosome 14 in B10.A (18R) mice is recombinant and includes Tcr-a alleles.  
A;Reference number: I54487; MUID:92165347; PMID:1371499  
A;Accession: I54487  
A;Status: preliminary; translated from GB/EMBL/DBD  
A;Molecule type: mRNA  
A;Residues: 1-120 <RES>  
A;Cross-references: UNIPROT:Q31213; GB:M55634; NID:G199677; PIDN:AAA39701.1; PID:G199678  
A;Accession: I68823  
A;Status: preliminary; translated from GB/EMBL/DBD  
A;Molecule type: mRNA  
A;Residues: 104-120 <RE2>  
A;Cross-references: GB:M55634; NID:G199677; PIDN:AAA39702.1; PID:G199679  
A;Note: J-alpha TA61  
C;Genetics:  
A;Gene: MHC-V-alpha-11; J-alpha-TA61  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: transmembrane protein  
F;26-100/Domain: immunoglobulin homology <IMM>

Query Match 9.9%; Score 101; DB 2; Length 120;  
Best Local Similarity 31.6%; Pred. No. 0.049;  
Matches 36; Conservative 17; Mismatches 47; Indels 14; Gaps 6;

QY 21 VSQPPERTL-EGSSAFPCSFNASQGLAIGSVTFRD-----EVVPGKEVRNGTPEFRG 75  
DB 14 VEQSPSALSHEGTDSALRCNFTTT-----MRSVQVFRKNRSGSLISLYLASGTKE-NG 67  
QY 76 RLAPLASSRFLHDHQAELHIRDVRGHDASIVCRVEVLGLGVT-GNGTRLVVE 128  
DB 68 RLKSAFDSK---ERYSTLHIRDAQLEDSTGYFCAADNTNGLTFGDGVLTWK 119

## RESULT 14

A24092  
T-cell receptor alpha chain V region (C.F6) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 21-Jan-2000  
C;Accession: A24092  
R;Pink, P.J.; Matis, L.A.; McElligott, D.L.; Bookman, M.; Hedrick, S.M.  
Nature 321, 219-226, 1986  
A;Title: Correlations between T-cell specificity and the structure of the antigen receptor  
A;Reference number: A93380; MUID:86230843; PMID:3012351  
A;Accession: A24092  
A;Molecule type: mRNA  
A;Residues: 1-110 <FIN>  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: T-cell receptor  
F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 9.8%; Score 100; DB 2; Length 110;  
Best Local Similarity 28.8%; Pred. No. 0.055;

Search completed: November 17, 2004, 00:20:13  
Job time : 40 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 17, 2004, 00:02:59 ; Search time 191 Seconds  
(without alignments)  
572.362 Million cell updates/sec

Title: US-10-036-444-2

Perfect score: 1020

Sequence: 1 MAMULLLIILVHVGSCALW.....GTHCHSDGPRGVPEPRCP 190

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 707533

Minimum DB seq length: 0

Maximum DB seq length: 190

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot\_02.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	916	89.8	180	1 NCT3_MACMU	Q8MJ02 macaca mulla
2	896	87.8	176	1 NCT3_MACFA	P61483 macaca fasc
3	109	10.7	172	2 Q71AM3	Q71AW3 bos taurus
4	109	10.7	172	2 AAQ10930	AAQ10930 bos taurus
5	106	10.4	132	1 TVA2_MOUSE	P01739 mus musculus
6	104	10.2	174	2 Q9Z1A7	Q9Z1A7 rattus norv
7	102.5	10.0	164	2 Q90XW9	Q90XW9 oreolobus
8	100	9.8	160	2 Q8TDA6	Q8TDA6 homo sapien
9	98.5	9.7	152	2 Q6LBN1	Q6LBN1 homo sapien
10	98.5	9.7	152	2 CAA39607	CAA39607 homo sapi
11	96	9.4	131	1 LV6E_HUMAN	P06319 homo sapien
12	95.5	9.4	164	2 Q90XX2	Q90XX2 oreolobus
13	91.5	9.0	108	2 Q8J25	Q8J25 oreolobus
14	91	8.9	167	2 BAC05245	BAC05245 homo sapi
15	90	8.8	178	2 Q9DJU4	Q9DJU4 mus musculus
16	89.5	8.8	137	2 Q9S653	Q9S653 homo sapien
17	89	8.7	142	1 VPR2_MOUSE	P13373 mus musculus
18	88.5	8.7	132	2 Q8TBD0	Q8TBD0 homo sapien
19	88	8.6	148	2 Q6PJ28	Q6PJ28 homo sapien
20	88	8.6	148	2 AAH23973	AAH23973 homo sapi
21	88	8.6	179	2 Q921X1	Q921X1 mus musculus
22	87.5	8.6	141	2 Q9NU66	Q9NU66 homo sapien
23	87.5	8.6	176	2 Q9NU65	Q9NU65 homo sapien
24	87.5	8.6	183	2 Q9NU64	Q9NU64 homo sapien
25	87	8.5	189	2 BAC86223	BAC86223 homo sapi
26	86.5	8.5	182	2 Q6JXL8	Q6JXL8 homo sapien
27	86.5	8.5	182	2 Q6X1E7	Q6X1E7 homo sapien
28	86	8.4	111	2 AAP49001	AAP49001 homo sapi
29	86	8.4	111	2 AAP86761	AAP86761 oreolobus
30	85.5	8.4	115	2 Q9B2K2	Q9B2K2 homo sapien
31	85	8.3	164	2 Q99KG0	Q99KG0 mus musculus

32 84 8.2 133 1 TVB2\_HUMAN  
33 83.5 8.2 135 2 Q90542  
34 83.5 8.2 164 2 Q90XW7  
35 83 8.1 134 1 TVB7\_MOUSE  
36 82.5 8.1 167 2 Q90XX1  
37 82 8.0 155 2 Q8TWX2  
38 82 8.0 167 2 Q90XW8  
39 80.5 7.9 142 2 Q9YHF2  
40 80 7.8 120 2 BAC00300  
41 80 7.8 142 1 VPR1\_MOUSE  
42 80 7.8 142 2 BAB27218  
43 80 7.8 142 2 BAB27242  
44 79.5 7.8 112 2 Q96JD2  
45 79.5 7.8 130 1 LV1G\_HUMAN

#### ALIGNMENTS

##### RESULT 1

NCT3\_MACMU STANDARD; PRT; 180 AA.  
AC Q8MJ02; Q8MJ00; Q8MJ01; Q95JB8;  
DT 05-JUL-2004 (Rel. 44, Created)  
DT 05-JUL-2004 (Rel. 44, Last sequence update)  
DT 01-OCT-2004 (Rel. 45, Last annotation update)  
DE Natural cytotoxicity triggering receptor 3 precursor (Natural killer cell p30-related protein) (Nkp30) (NK-p30).  
DE cell p30-related protein) (Nkp30) (NK-p30).  
GN Name=NCR3;  
OS Macaca mulatta (Rhesus macaque).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Macaca.  
OC Cercopithecoidea; Macaca.  
OX NCBI\_TaxID=9544;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4), AND VARIANT VAL-156.  
RA Labonte M.L., Miller J., Letvin N.L.;  
RT "Molecular cloning of rhesus monkey Nkp46 and Nkp30 and identification of Nkp46SD and Nkp30S".  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 4), AND VARIANT VAL-156.  
RC TISSUE=Lymphoid;  
RA Rizzi M., Biassoni R.;  
RT "NCR express by macaca NK cells.";  
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Cytotoxicity activating receptor that may contribute to the increased efficiency of activated natural killer (NK) cells to mediate tumor cell lysis (By similarity).  
CC -!- SUBUNIT: Interacts with CD3z (By similarity).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=4;  
CC Name=1;  
CC IsoId=Q8MJ02-1; Sequence=Displayed;  
CC Note=No experimental confirmation available;  
CC Name=2;  
CC IsoId=Q8MJ02-2; Sequence=VSP\_010414;  
CC Note=No experimental confirmation available;  
CC Name=3;  
CC IsoId=Q8MJ02-3; Sequence=VSP\_010415, VSP\_010416;  
CC Note=No experimental confirmation available;  
CC Name=4;  
CC IsoId=Q8MJ02-4; Sequence=VSP\_010417;  
CC Note=No experimental confirmation available;  
CC -!- SIMILARITY: Belongs to natural cytotoxicity receptor (NCR) family.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial



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DE EMBL: AF539438; AAQ10930.1; -.
DR InterPro; IPR008096; CTLA4.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG. 1.
DR PRINTS; PR01720; CTLANTIGEN4.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
SQ SEQUENCE 172 AA; 18972 MW; 7F53F5928EFA39E4 CRC64;

Query Match 10.7%; Score 109; DB 2; Length 172;
Best Local Similarity 25.6%; Pred. No. 0.088;
Matches 43; Conservative 22; Mismatches 69; Indels 34; Gaps 5;

QY 6 LLILIMVHPSGSCALWVSQPPPEIRTLGSSAFPLCSFNASQGRLAIGSVTFRDEVVPGKE 65
DB 23 LFFLVTFIPVFSKGMNVTQPPVLLASSRGVASFCEYESS-GRADVRVTVLREAGSQVTE 81
QY 66 VRNGTPEFRGLAPLASSRFL--HDHQAEHLHVRDVRGHDAIYVCRVEVL--GLGVGT 119
DB 82 VCAGTVNVEDLFLDDSTCIGTSRGKNKVNLTIQGLRAMDTGLYVCKVELMYPPIYVGI 141
QY 120 GNGTRL-VVEKEHPQLGAGTVLLLRAGFVAVSFLSVAGSTVYQKGC 166
DB 142 GNGTQIVYIAKEK-----KPSYIRGLC 163

RESULT 4
AAQ10930 PRELIMINARY; PRT; 172 AA.
AC AAQ10930;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE CTLA-4 isoform 1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Ann J.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF539438; AAQ10930.1; -.
SQ SEQUENCE 172 AA; 18972 MW; 7F53F5928EFA39E4 CRC64;

Query Match 10.7%; Score 109; DB 2; Length 172;
Best Local Similarity 25.6%; Pred. No. 0.088;
Matches 43; Conservative 22; Mismatches 69; Indels 34; Gaps 5;

QY 6 LLILIMVHPSGSCALWVSQPPPEIRTLGSSAFPLCSFNASQGRLAIGSVTFRDEVVPGKE 65
DB 23 LFFLVTFIPVFSKGMNVTQPPVLLASSRGVASFCEYESS-GRADVRVTVLREAGSQVTE 81
QY 66 VRNGTPEFRGLAPLASSRFL--HDHQAEHLHVRDVRGHDAIYVCRVEVL--GLGVGT 119
DB 82 VCAGTVNVEDLFLDDSTCIGTSRGKNKVNLTIQGLRAMDTGLYVCKVELMYPPIYVGI 141
QY 120 GNGTRL-VVEKEHPQLGAGTVLLLRAGFVAVSFLSVAGSTVYQKGC 166
DB 142 GNGTQIVYIAKEK-----KPSYIRGLC 163

RESULT 5
TVA2 MOUSE
ID TVA2 MOUSE STANDARD; PRT; 132 AA.
AC P01739;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)

```

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DE T-cell receptor alpha chain V region 2B4 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (CLONE TT11).
RX MEDLINE=85036634; PubMed=6548551;
RA Chien Y., Becker D.M., Lindsten T., Okamura M., Cohen D.I.,
RA Davis M.M.;
RT "A third type of murine T-cell receptor gene.";
RL Nature 312:31-35(1984).
DR PIR; A02015; RWSAV.
DR HSSP; P01738; ITCR.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Glycoprotein; Immunoglobulin domain; Receptor; Signal; T-cell.
FT CHAIN 1 20 T-cell receptor alpha chain V region 2B4.
FT DOMAIN 21 132 V segment.
FT DOMAIN 114 117 D segment.
FT DOMAIN 118 132 J segment.
FT CARBOHYD 42 42 N-linked (GlcNAc...).
FT NON_TER 132 132
SQ SEQUENCE 132 AA; 14668 MW; CABBF6CFIDD3448B CRC64;

Query Match 10.4%; Score 106; DB 1; Length 132;
Best Local Similarity 25.8%; Pred. No. 0.12;
Matches 40; Conservative 22; Mismatches 45; Indels 48; Gaps 9;

QY 3 WLLILLIMVHPSGSCALWVS-----QPPEIRTLGSSAFPLCSFNASQGRLAIGSVTW 55
DB 12 WLLL-----NWNVSQNVQSPESLIPEGARTSLNCTFDSASQY----FWW 55
QY 56 PRDEVVPGKEVR-----NGTPEFRGLAPLASSRFLHDAHLHVRDVRGHDAIYVC 108
DB 56 YRQH--SGKAPKALMSIFSNGEKE-EGRTFHLNKAHLH--FSLHSDSQPSDLSALYLC 109
QY 109 RVEVLGLGVGTGNGTFLVVEKEHPQLGAGTVLLLR 143
DB 110 AVTYIG-----GSGNKLI-----FGTGILLSVK 132

RESULT 6
Q9Z1A7 PRELIMINARY; PRT; 174 AA.
AC Q9Z1A7;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CTLA-4.
GN Name=CTLA-4;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ACI;
RA Oaks M.K.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U90271; AAD00697.1; -.
DR HSSP; P09793; 1DQT.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR008096; CTLA4.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG; 1.
DR PRINTS; PR01720; CTLANTIGEN4.

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